Canadian Patents Database

Search Results

03/29/2004 - 15:46:13

Search Query :

((oligonucleotide library, randon sequences, fixed sequences or defined

Query: ((oligonucleotide library, randon sequences, fixed sequences or defined sequences))

28 documents out of 1589578 matched your query. Click on its number to view the details of the document.

Note: All document detail pages now appear on a new Browser Window.

1.	2267524	IDENTIFYING ANTISENSE OLIGONUCLEOTIDE BINDING	47%
2.	2084411	PEPTIDE LIBRARY AND SCREENING SYSTEMS	47%
3.	2436519	SELECTION OF CATALYTIC NUCLEIC ACIDS TARGETED TO INFECTIOUS AGENTS	41%
4.	2418724	TARGET ACTIVATED NUCLEIC ACID BIOSENSOR AND METHODS OF USING SAME	41%
5.	2401320	RANDOM TRUNCATION AND AMPLIFICATION OF NUCLEIC ACID	41%
6.	2141450	METHOD FOR INTRODUCING DEFINED SEQUENCES AT THE 3' END OF POLYNUCLEOTIDES	41%
7.	2103000	METHOD FOR PROMOTING SPECIFIC ALIGNMENT OF SHORT OLIGONUCLEOTIDES ON NUCLEIC ACIDS	41%
8.	1070845	FUNCTION MULTIPLEXER	41%
9.	2445884	ELUCIDATION OF GENE FUNCTION	40%
10.	2326408	EPITOPE PEPTIDES IMMUNOGENIC AGAINST STREPTOCOCCUS PNEUMONIAE	40%
11.	2284481	METHOD OF PRODUCING A SUBTRACTION LIBRARY	40%

12.	2125004	SIMULTANEOUS AMPLIFICATION OF MULTIPLE TARGETS	40%
13.	2440649	METHOD TO SCREEN PEPTIDE DISPLAY LIBRARIES USING MINICELL DISPLAY	39%
14.	2439263	THREE HYBRID ASSAY SYSTEM	39%
15.	2435361	COMMUNICATION METHOD AND A HEARING AID SYSTEM	39%
16.	2405715	METHODS FOR SELECTIVE TARGETING	39%
17.	2397844	METHOD FOR ANALYZING NUCLEIC ACID SEQUENCES	39%
18.	2386070	METHOD AND APPARATUS FOR SORTING ITEMS OF MAIL	39%
19.	2376421	IDENTIFICATION AND MOLECULAR CHARACTERISATION OF PROTEINS, EXPRESSED IN THE TICK SALIVARY GLANDS	39%
20.	2360567	PROCESS FOR THE GENERATION OF OLIGONUCLEOTIDE LIBRARIES (OLS) REPRESENTATIVE OF GENOMES OR EXPRESSED MRNAS (CDNAS) AND USES THEREOF	39%
21.	2255673	PROMOTER ELEMENTS CONFERRING ROOT-PREFERRED GENE EXPRESSION	39%
22.	2251464	NON-DENDRITIC BACKBONE PEPTIDE CARRIER	39%
23.	2194558	CONJUGATES MADE OF METAL COMPLEXES AND OLIGONUCLEOTIDES	39%
24.	2183643	PRODUCTS COMPRISING SUBSTRATES CAPABLE OF ENZYMATIC CROSS-LINKING	39%
25.	2128528	PROCESS FOR TYPING OF HCV ISOLATES	39%
26.	2099020	APPARATUS AND METHOD FOR CREATION OF A USER DEFINABLE VIDEO DISPLAYED DOCUMENT SHOWING CHANGES IN REAL TIME DATA	39%
27.	1253974	PREDEFINED CHARACTER SEQUENCE GENERATOR	39%
28.	1235479	VARIABLE RESOLUTION SCANNING IN LINE SCAN OPTICAL IMAGING SYSTEMS	39%

Last Modified: 2002-12-31 ▲ Important Notices

NL OA PT SD SE SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK
DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT
RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZM ZW
AU 2002028756 A 20020618 (200262)
EP 1353935 A2 20031022 (200370) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
RO SE SI TR

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002046449	A2	WO 2001-US46178	20011207
AU 2002028756	A	AU 2002-28756	20011207
EP 1353935	A2	EP 2001-989871	20011207
		WO 2001-US46178	20011207

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2002028756	A	Based on	WO 2002046449
EP 1353935	A2	Based on	WO 2002046449

PRIORITY APPLN. INFO: US 2000-251810P 20001207
AN 2002-519672 [55] WPIDS
CR 2000-638570 [61]; 2001-607700 [69]
AB WO 200246449 A UPAB: 20031030
NOVELTY - Identifying (M) one or more cleavage sites in a target RNA which are accessible to a ribozyme (Rz), DNAzyme (Dz), antisense **oligonucleotide** (ASO) involves generating **libraries** of Rzs, Dzs and ASOs, where Rzs and Dzs comprise a catalytic core **flanked** by **random** nucleotides. A target RNA is added to the library of nucleic acids and nucleic acids that bind to and/or cleave the target RNA are isolated.

DETAILED DESCRIPTION - Cleavage sites in a target RNA which are accessible to a Rz are identified by generating a library of RNAs, where each RNA in the library comprises a catalytically active hammerhead Rz core **flanked** on each side by **random** nucleotide regions, where the nucleotide regions are **flanked** on each side by **fixed** sequences which allow **amplification** and a sequence which allow transcription of the RNA. The target RNA is contacted with the library of RNAs under conditions in which the Rz core is not catalytically active, and RNAs that binds to the target RNA are separated from RNAs that do not bind. An enriched library of RNAs comprising bound RNAs is generated and the steps are repeated at least one additional time with a reduced ratio of the target RNA to the library of RNAs. 5' or 3' end-labeled target RNA is generated and contacted with enriched library of RNAs such that the target RNA is cleaved to produce cleavage products, the cleavage products are separated and the sequence or sequences at which cleavage of the end-labeled target RNA occurred as a result of incubation of the end-labeled target RNA with the library of RNAs, is determined.

Identifying cleavage sites in target RNA which are accessible to Dz, involves generating a library of Dzs, where the Dz core is **flanked** on each side by **random** nucleotide regions which are limited to not more than seven **random** nucleotides upstream of the Dz core and not more than eight **random** nucleotides downstream of the Dz

(1997), 36(12), 1321-1324
CODEN: ACIEAY; ISSN: 0570-0833
PUBLISHER: Wiley-VCH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB 3'-5'-Phosphoramidate bond-containing DNA sequences capable of catalyzing cofactor-assisted self-cleavage were obtained by in vitro selection from an **oligonucleotide library** containing a **randomized** 72-mer sequence. The method involved preparation of immobilized phosphoramidate-containing **randomized** 72-mer. The 72-mer was then allowed to react in presence of dansylated trimer, hexameric template, and magnesium. Reaction produced a pool of catalytic 72-mers which was amplified for the next round of selection. Neg. selection (removal of those DNA sequences that were released via uncatalyzed hydrolysis) was also utilized. Cloning and sequencing of **PCR** products from the last rounds revealed a single dominating clone. The secondary structure was predicted and showed tight folding around the constant primer regions. Closer examination of the cloned sequence showed that it catalyzes the hydrolysis (not transphosphorylation) of an internal 3'-5'-phosphoramidate bond in the presence of a specific trimeric cofactor.

REFERENCE COUNT: 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 77 OF 89 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 97:206647 SCISEARCH
THE GENUINE ARTICLE: WL606
TITLE: Mapping sequence specific DNA-protein interactions: A versatile, quantitative method and its application to transcription factor XF1
AUTHOR: Luo B; Perry D J; Zhang L I; Kharat I; Basic M; Fagan J B (Reprint)
CORPORATE SOURCE: MAHARISHI UNIV MANAGEMENT, MOL BIOL LAB, FAIRFIELD, IA 52557 (Reprint); MAHARISHI UNIV MANAGEMENT, MOL BIOL LAB, FAIRFIELD, IA 52557
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF MOLECULAR BIOLOGY, (28 FEB 1997) Vol. 266, No. 3, pp. 479-492.
Publisher: ACADEMIC PRESS LTD, 24-28 OVAL RD, LONDON, ENGLAND NW1 7DX.
ISSN: 0022-2836.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 46

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB We have developed a method for the quantitative, exhaustive Sequence Specificity determination of DNA-binding proteins. The QuESSD method overcomes the limitations inherent in other published in vitro selection methods, not only defining the consensus sequence, but also quantifying the effect on DNA-protein affinity of replacing each base in the recognition domain with every other base. The features distinguishing this method from other in vitro selection approaches are: (1) instead of synthesizing one target oligonucleotide population containing a long **randomized** domain, we synthesize several oligonucleotide populations, each **randomized** at two positions. (2) Instead of carrying out several cycles of selection and **amplification** we carry out a single cycle. (3) We have developed data collection and analysis procedures that eliminate artifacts and allow generation of quantitative results. The QuESSD method yields accurate measures of: (a)

US 1996-650400 A2 19960520
WO 1996-US19256 W 19961202
US 1999-239395 A 19990128

AB A method for DNA reassembly after **random** fragmentation, and its application to mutagenesis of nucleic acid sequences by in vitro or in vivo recombination is described. In particular, a method for the production of nucleic acid fragments or polynucleotides encoding mutant proteins is described. The present invention also relates to a method of repeated cycles of mutagenesis, shuffling and selection which allow for the directed mol. evolution in vitro or in vivo of proteins. Using these methods Aequoreas victorias green fluorescent protein was mutagenized to a form with a 45-fold improvement in fluorescence signal. The DNA shuffling method, when applied to arsenate detoxification bacteria, improved arsenate resistance 50-100-fold.

L21 ANSWER 75 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:735877 HCAPLUS
DOCUMENT NUMBER: 128:10869
TITLE: Identification of oligonucleotide ligands for biomolecules for diagnostic, therapeutic, or research use from completely **random** libraries
INVENTOR(S): Bruice, Thomas W.; Lima, Walter F.
PATENT ASSIGNEE(S): ISIS Pharmaceuticals, Inc., USA
SOURCE: U.S., 22 pp., Cont.-in-part of U.S. Ser. No. 755,485, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5686242	A	19971111	US 1994-330000	19941027
US 6022691	A	20000208	US 1997-965908	19971107

PRIORITY APPLN. INFO.: US 1991-755485 19910905
WO 1992-US7489 19920904
US 1994-330000 19941027

AB Oligonucleotides that selectively bind to target biomols. are determined by in vitro assay of a pool of **random** oligonucleotides for their binding to the target biomol. followed by recovery and characterization of selected oligonucleotides. The oligonucleotides have as large a **random** sequence as possible and may be completely **random** or may have a 5'-poly(A) tail that can be used for oligo(dT)-directed formation of a cDNA followed by **PCR** amplification of the products. The binding and sequence of the oligonucleotide may then be characterized by affinity cleavage. These oligonucleotides may be used for therapeutic, diagnostic and research reagent purposes.

L21 ANSWER 76 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:454756 HCAPLUS
DOCUMENT NUMBER: 127:202056
TITLE: Cofactor-assisted self-cleavage in DNA libraries with a 3'-'5'-phosphoramidate bond
AUTHOR(S): Burmeister, Jens; von Kiedrowski, Gunter; Ellington, Andrew D.
CORPORATE SOURCE: Lehrstuhl Organische Chemie I Universitat, Bochum, D-44801, Germany
SOURCE: Angewandte Chemie, International Edition in English

Search completed by David Schreiber 308-4292

the selectivity of the protein for each base at each position within the recognition domain (normalized relative selectivity), (b) the contributions of individual sites within the recognition domain to the binding affinity (selectivity **variance**), (c) the relative binding affinity of any given sequence (global selectivity). We confirmed results by (1) tabulating directly the frequency of appearance of individual species in the pool of protein-bound oligonucleotides by cloning and sequencing individual oligonucleotides, and (2) competition EMSA analysis of oligonucleotides designed on the basis of QuESSD data. We have used this method to map the sequence specificity of the nuclear protein XF1 and to distinguish the sequence specificities of XF1 and the AH receptor complex, both of which bind to XRE1, a xenobiotic responsive element (XRE) located upstream of the CYP1A1 gene. Using data obtained by the QuESSD method, we designed oligonucleotides specific for XF1 or for the AH receptor, and prepared CAT reporter gene constructs carrying these oligonucleotides, or wild-type XRE1, upstream of a minimal promoter. Transfection studies using these constructs indicated that XF1 can function as a weak activator of basal transcription, and can, under some circumstances, compete with the AH receptor for binding to XRE1. (C) 1997 Academic Press Limited.

L21 ANSWER 78 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:113789 HCAPLUS
DOCUMENT NUMBER: 126:166968
TITLE: Long-inverse **PCR** to generate regional peptide libraries by codon mutagenesis
AUTHOR(S): Eisinger, Dominic P.; Trumpower, Bernard L.
CORPORATE SOURCE: Dartmouth Medical School, Hanover, NH, USA
SOURCE: BioTechniques (1997), 22(2), 250-254
CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER: Eaton
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Here we describe a method to construct protein libraries by codon mutagenesis, which can be applied to any gene encoded by a plasmid without the need for restriction sites and subcloning. The four steps of the method include: long-inverse **PCR** with two primers (one of which is **randomized**), removal of the 3'-overhangs with T4 DNA polymerase, phosphorylation of the 5' termini and self ligation to regenerate a plasmid **library** incorporating the **randomized oligonucleotide** pool.

L21 ANSWER 79 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:646701 HCAPLUS
DOCUMENT NUMBER: 127:342371
TITLE: Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library
AUTHOR(S): Suzuki, Yutaka; Yoshitomo-Nakagawa, Kiyomi; Maruyama, Kazuo; Suyama, Akira; Sugano, Sumio
CORPORATE SOURCE: International and Interdisciplinary Studies, The University of Tokyo, 3-8-1, Komaba, Meguro-ku, Tokyo, Japan
SOURCE: Gene (1997), 200(1-2), 149-156
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Using 'oligo-capped' mRNA (Maruyama, K., Sugano, S., 1994), whose cap structure was replaced by a synthetic oligonucleotide, we constructed two

LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO,
RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 6544741	B1	20030408	US 2000-614614		20000712
AU 2001079989	A5	20020618	AU 2001-79989		20010711
PRIORITY APPLN. INFO.:			US 2000-614614	A	20001207
			WO 2001-IB1343	W	20010711

AB This invention provides methods for constructing a normalized cDNA library, constructing a low copy gene library, preparing a probe from a biol. sample and a kit for constructing a normalized cDNA library. The method for constructing a normalized cDNA **library** involves identifying and synthesizing **oligonucleotides** complementary to the 3' poly-A region of target mRNA. RNA-DNA heteroduplexes formed between target RNA and said primers are cleaved using RNase H. Oligo(dT) or oligo(dU) primers containing a first restriction endonuclease recognition site are used to prime synthesis of first strand cDNA by reverse transcription. Furthermore, a second strand cDNA is generated to produce double-stranded cDNA. Adapters (with cohesive ends of a second restriction endonuclease) are ligated to both ends of the double-stranded cDNA. The second restriction endonuclease site is different from the first one. Double-stranded cDNA fragments less than 150 bp are removed by gel electrophoresis. The remaining cDNA mols. are digested with the first restriction endonuclease, followed by digestion with the second restriction endonuclease. The remaining cDNA mols. are cloned into a vector, predigested with the first and second restriction endonuclease to permit cloning of only the non-target cDNAs. The mRNA may be selected from animals, plants, bacteria or viruses. A method of constructing a low copy gene library involves synthesizing a short first strand cDNA extension on a first RNA using **random** or oligo(dT) primers. The RNA mols. are cleaved and the short first strand cDNA are purified. The cDNA extensions are annealed with the 3' poly-A end of a second RNA to form a heteroduplex. RNAase H is used to cleave the RNA in the heteroduplex and the cDNA-RNA duplex is denatured. The steps of annealing second RNA mols. to cDNA extensions and cleavage by RNAase H, at a temperature between 37-42°C, are repeated following denaturation of the cDBA-RNA duplex at a temperature between 65-75°C. CDNA is then synthesized from the remaining RNA and cloned into a plasmid vector like the pQ vector. In normalization methods, the first and second RNA mols. are from the same source but differ in the **subtraction** method.

L21 ANSWER 16 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:241008 HCAPLUS
DOCUMENT NUMBER: 136:289892
TITLE: High throughput screening of mRNAs for areas accessible to antisense oligonucleotides
INVENTOR(S): Liang, Zicai; Zhang, Hong-Yan; Wahlestedt, Claes
PATENT ASSIGNEE(S): Neuromics Inc., USA
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

Wilder 09/869,891

WO 2002024950 A2 20020328 WO 2001-SE2054 20010925
WO 2002024950 A3 20021205
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
US 2002187482 A1 20021212 US 2001-961700 20010924
AU 2001092468 A5 20020402 AU 2001-92468 20010925
PRIORITY APPLN. INFO.: US 2000-235029P P 20000925
WO 2001-SE2054 W 20010925

AB This invention relates to methods for identifying regions of RNA mols. that are available for interaction with small mols., particularly regions that can hybridize with oligonucleotides having complementary sequences. Identifying such regions is useful in the design of probes, anti-sense oligonucleotides and small mol. drugs. The method involves using a **library** of **oligonucleotides** with a **randomized** core sequence and constant **flanking** regions. The constant regions may be blocked with blocking oligonucleotides to prevent non-specific hybridization. Sequences are hybridized to immobilized mRNAs under conditions in which the mRNA maintains its folded conformation. Sequences hybridizing to the mRNA are then amplified by **PCR** using the constant regions. Sequencing of the amplification products identifies the exposed regions of the mRNA that may be targeted, e.g by antisense oligonucleotides. The method is demonstrated by anal. of the accessible regions of the rabbit β-globin mRNA.

L21 ANSWER 17 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:220779 HCAPLUS
DOCUMENT NUMBER: 136:258268
TITLE: Combinatorial screening of libraries from mixed populations of organisms for the identification of novel biologically active substances
INVENTOR(S): Short, Jay M.
PATENT ASSIGNEE(S): Diversa Corporation, USA
SOURCE: PCT Int. Appl., 154 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 40
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002022810	A2	20020321	WO 2001-US29712	20010917
WO 2002022810	A3	20030227		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

Search completed by David Schreiber 308-4292

AU 756201	B2	20030109	AU 2000-48933	20000731
AU 2000048933	A5	20001005		
US 2002086279	A1	20020704	US 2001-875412	20010606
US 6677115	B2	20040113		
AU 2001091208	A5	20020326	AU 2001-91208	20010917
EP 1319068	A2	20030618	EP 2001-971309	20010917

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

PRIORITY APPLN. INFO.:
US 2000-663620 A2 20000915
AU 1997-11489 A3 19961206
US 1997-988224 A1 19971210
WO 2001-US29712 W 20010917

AB Provided is a method of screening gene libraries derived from a mixed population of organisms for a bioactivity of biomol. of interest. The mixed population of organisms can be a cultured population or an uncultured population from, for example, the environment. Also provided are methods of screening isolates or enriched populations of organisms, which isolates include a population that is spatially, temporally, or hierarchical, for example, of a particular species, genus family, or class of organisms. Identified clones containing a biomol. or bioactivity of interest can be further variegated or the DNA contained in the clone can be variegated to create novel biomols. or bioactivities of interest.

L21 ANSWER 18 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:157994 HCAPLUS
DOCUMENT NUMBER: 136:195290
TITLE: Massive mutagenesis: large-scale site-directed mutagenesis with high yield of mutants using **oligonucleotide libraries**
INVENTOR(S): Delcourt, Marc; Blesa, Stephane
PATENT ASSIGNEE(S): Biomethodes, Fr.
SOURCE: PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: French
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002016606	A2	20020228	WO 2001-FR2666	20010824
WO 2002016606	A3	20020627		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

FR 2813314	A1	20020301	FR 2000-10962	20000825
AU 2001086009	A5	20020304	AU 2001-86009	20010824
EP 1311670	A2	20030521	EP 2001-965350	20010824

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

JP 2004507243	T2	20040311	JP 2002-522277	20010824
US 2004048268	A1	20040311	US 2003-362576	20030806

PRIORITY APPLN. INFO.:
FR 2000-10962 A 20000825

Search completed by David Schreiber 308-4292

WO 2001-FR2666 W 20010824

AB The invention concerns the field of mol. biol. and more particularly that of mutagenesis. It concerns a method of high-rate directed mutagenesis, that is the formation of numerous directed mutants in reduced time and with reduced number of steps. The method, which combines the advantages of site-directed and **random** mutagenesis, is referred to as massive mutagenesis. The method uses mutagenic oligonucleotides that have conserved **flanking** regions that direct them to a target sequence and a central region containing one or more mutagenic bases. The oligonucleotide panels preferably contains 50-500 members, although it may contain 5-106 members.

L21 ANSWER 19 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:123272 HCAPLUS
DOCUMENT NUMBER: 136:162314
TITLE: Methods for identifying low-abundance polynucleotides and related compositions
INVENTOR(S): Zhu, York Yuan-Yuan
PATENT ASSIGNEE(S): Genemed Biotechnologies, Inc., USA
SOURCE: PCT Int. Appl., 99 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002012564	A2	20020214	WO 2001-US24730	20010806
WO 2002012564	A3	20031224		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 6465219	B1	20021015	US 2000-632898	20000807
AU 2001083159	A5	20020218	AU 2001-83159	20010806
EP 1395678	A2	20040310	EP 2001-961937	20010806
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2004006033	A1	20040108	US 2003-343345	20030630

PRIORITY APPLN. INFO.: US 2000-632898 A1 20000807
US 2001-288777P P 20010504
WO 2001-US24730 W 20010806

AB This invention provides novel methods for producing a plurality of polynucleotides prepared from a polynucleotide sample and the plurality of polynucleotides so produced. In one embodiment, the plurality of polynucleotides is prepared by **subtractive** hybridization between test and reference polynucleotide samples and is substantially enriched in sequences that are either not present in the reference polynucleotide sample or are present in the reference polynucleotide sample in substantially lower concentration than in the test polynucleotide sample. The plurality of polynucleotides is also substantially enriched in low-abundance sequences, relative to the test polynucleotide sample. In preferred embodiments, the test and reference polynucleotide samples are selected from mRNA from first and

second cell or tissue; mRNA form cell or tissue at different stage of development; mRNA from cell or tissue treated or untreated with active agent; mRNA normal and diseased cell or tissue. The invention also provides kits useful in the methods of the invention and for using the polynucleotides produced thereby. The polynucleotides are useful in a wide variety of applications, such as cloning, expression, and hybridization studies.

L21 ANSWER 20 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:72312 HCAPLUS
DOCUMENT NUMBER: 136:129908
TITLE: Modified SELEX method for photoselecting nucleic acid ligands to fibroblast growth factor-2 (bFGF) and diagnostic uses
INVENTOR(S): Gold, Larry; Smith, Jonathan Drew; Koch, Tad; Golden, Mace
PATENT ASSIGNEE(S): Somalogic, Inc., USA
SOURCE: PCT Int. Appl., 105 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 127
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002006510	A2	20020124	WO 2001-US22561	20010718
WO 2002006510	A3	20020606		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 6458539	B1	20021001	US 2000-619213	20000719
AU 2001073548	A5	20020130	AU 2001-73548	20010718

PRIORITY APPLN. INFO.:

US 2000-619213	A	20000719
US 1993-123935	B2	19930917
US 1996-612895	A2	19960308
US 1998-93243	A2	19980608
US 1999-459553	A2	19991213
WO 2001-US22561	W	20010718

AB The invention provides a modified SELEX method, termed PhotoSELEX, an acronym for Photochem. Systematic Evolution of Ligands by EXponential enrichment. PhotoSELEX identifies and selects high-affinity single strand DNA (ssDNA) ligands capable of binding and/or photocrosslinking to bFGF by screening a **random** 61-mer **oligonucleotide library** in which 5-bromo-2'-deoxyuridine replaced thymidine was completed against bFGF target. This invention also provides two modified high-affinity ssDNA ligands capable of photocrosslinking bFGF ligands to bFGF which exhibited high sensitivity for bFGF comparable to that of com. available ELISA monoclonal antibodies with an absolute sensitivity of at least 0.058 ppt bFGF under prevailing test conditions. Addnl., the ligands were able to distinguish bFGF from consanguine proteins, vascular endothelial growth factor and platelet derived growth factor and from other proteins in serum. Further included is a method for determining the exact position of

the photocrosslink between the nucleic acid ligand and the target mol.

L21 ANSWER 21 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2002:278539 BIOSIS
DOCUMENT NUMBER: PREV200200278539
TITLE: Chimeric oligonucleotides and uses thereof in the identification of antisense binding sites.
AUTHOR(S): Schmidt, Gunter [Inventor, Reprint author]
CORPORATE SOURCE: Cambs, UK
ASSIGNEE: Xzillion GmbH and Co. KG, Frankfurt, Germany
PATENT INFORMATION: US 6355418 March 12, 2002
SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Mar. 12, 2002) Vol. 1256, No. 2. http://www.uspto.gov/web/menu/patdata.html. e-file. CODEN: OGUPE7. ISSN: 0098-1133.
DOCUMENT TYPE: Patent
LANGUAGE: English
ENTRY DATE: Entered STN: 8 May 2002
Last Updated on STN: 8 May 2002

AB A chimaeric **oligonucleotide library** for use in identifying an antisense binding site in a target mRNA, comprising a plurality of distinct chimaeric oligonucleotides capable of hybridizing to mRNA to form a duplex, the nucleotide sequences of which each have a common length of 7 to 20 bases and are generated **randomly** or generated from information characterizing the sequence of the target mRNA, wherein substantially all the nucleotide sequences of said common length which are present as sub-sequences in the target mRNA are present in the library, and wherein each nucleotide sequence comprises: a) a recognition region comprising a sequence of nucleotides which is recognizable by a duplex-cutting RNAase when hybridized to the mRNA, and b) a **flanking** region comprising a sequence of chemically-modified nucleotides which binds to the mRNA sufficiently tightly to stabilize the duplex for cutting of the mRNA in the duplex by the duplex-cutting RNAase, wherein the nucleotides constituting the **flanking** region are different from those constituting the recognition region, and wherein each oligonucleotide is protected against exonuclease attack.

L21 ANSWER 22 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2003-093136 [08] WPIDS
CROSS REFERENCE: 2000-206001 [18]; 2003-219980 [21]; 2003-730171 [69]
DOC. NO. CPI: C2003-023382
TITLE: Template-mediated, ligation-oriented method for **randomly** shuffling polynucleotide (e.g. DNA shuffling), genetic recombination or molecular breeding, by adjacently hybridizing at least two fragments on an assembly template.
DERWENT CLASS: B04 D16
INVENTOR(S): DUPRET, D; LEFEVRE, F; MASSON, J M; MASSON, J
PATENT ASSIGNEE(S): (PROT-N) PROTEUS SA; (DUPR-I) DUPRET D; (LEFE-I) LEFEVRE F; (MASS-I) MASSON J; (PROT-N) PROTEUS
COUNTRY COUNT: 101
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002086121	A1	20021031	(200308)*	EN	73

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK

Search completed by David Schreiber 308-4292

DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR
KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT
RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM
ZW
FR 2824073 A1 20021031 (200308)
US 2003215800 A9 20031120 (200377)
EP 1381680 A1 20040121 (200410) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
RO SE SI TR

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2002086121	A1		WO 2002-IB2778	20020425
FR 2824073	A1		FR 2001-5573	20010425
US 2003215800	A9	Cont of	WO 1999-FR1973	19990811
		CIP of	US 2000-723316	20001128
			US 2001-840861	20010425
EP 1381680	A1		EP 2002-743543	20020425
			WO 2002-IB2778	20020425

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1381680	A1	Based on	WO 2002086121

PRIORITY APPLN. INFO: US 2001-840861 20010425; FR 2001-5573 20010425; US 2001-285998P 20010425; FR 1998-10338 19980812

AN 2003-093136 [08] WPIDS

CR 2000-206001 [18]; 2003-219980 [21]; 2003-730171 [69]

AB WO 200286121 A UPAB: 20040210

NOVELTY - A template-mediated, ligation-oriented method for **randomly** shuffling polynucleotides comprising adjacently hybridizing at least two fragments on an assembly template, is new.

DETAILED DESCRIPTION - A template-mediated, ligation-oriented method (M1) for **randomly** shuffling polynucleotides comprises:

(a) obtaining, directly or indirectly, from a **polynucleotide library**, single-stranded fragments of at least two homologous polynucleotides;

(b) hybridizing the fragments to one or more devised assembly templates until at least two of the fragments are adjacently hybridized to form at least one partially double-stranded polynucleotide, where at least one of the templates shares at least one zone of homology with the homologous polynucleotide;

(c) treating the partially double-stranded polynucleotide, in order to form at least one recombinant polynucleotide, by:

(i) ligating nicks; and

(ii) where necessary, any one of or any combination of the following:

(1) filling in gaps by further hybridizing the fragments to the templates to increase the number of fragments that are adjacently hybridized;

(2) filling in short gaps by trimming any overhanging flaps of any partially hybridized fragments; or

(3) filling in short gaps via polymerization.

INDEPENDENT CLAIMS are also included for the following:

(1) a template-mediated, ligation-oriented method for in vitro non-

random shuffling of mutation-containing zones of polynucleotides comprising the steps of the new method above;
(2) a template-mediated, ligation-oriented method for in vitro non-**random** low-homology shuffling of gene families the steps of the new method above;
(3) a recombinant polynucleotide obtained by the method;
(4) a vector comprising the polynucleotide;
(5) a cellular host transformed by the polynucleotide;
(6) a protein encoded by the polynucleotide;
(7) **libraries** comprising the recombinant **polynucleotide**, vector, cellular host or protein;
(8) a physical array in which the method can be performed; and
(9) logical arrays that stimulate the method or the physical array above;
(10) (in vitro) polynucleotide shuffling reaction mixtures comprising:
(a) (free) single-stranded fragments of at least two homologous polynucleotides; and
(b) at least one devised assembly template upon which at least two of the (restriction) fragments can hybridize adjacently.
USE - The method is useful for generating novel polynucleotides that differ in some advantageous respect compared to a reference sequence. These methods are particularly useful in genetic recombination, e.g. in directed evolution, molecular breeding or DNA shuffling.
Dwg.0/16

L21 ANSWER 23 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2003-058524 [05] WPIDS
DOC. NO. CPI: C2003-015019
TITLE: Preparing a **library** of **polynucleotides** by contacting a parent set of polynucleotides with at least 1 class IIS restriction enzyme with sites capable of being cleaved by IIS restriction enzyme to from polynucleotide fragments.
DERWENT CLASS: B04 D16
INVENTOR(S): DELAGRAVE, S
PATENT ASSIGNEE(S): (DELA-I) DELAGRAVE S; (HERC) HERCULES INC
COUNTRY COUNT: 101
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002081643	A2	20021017	(200305)*	EN	45
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG UZ VN YU ZA ZM ZW					
US 2003087254	A1	20030508	(200337)		
EP 1383910	A2	20040128	(200409)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002081643	A2	WO 2002-US10905	20020404

Search completed by David Schreiber 308-4292

US 2003087254	A1	Provisional	US 2001-281587P 20010405
			US 2002-114379 20020402
EP 1383910	A2		EP 2002-763977 20020404
			WO 2002-US10905 20020404

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1383910	A2	Based on	WO 2002081643

PRIORITY APPLN. INFO: US 2002-114379 20020402; US 2001-281587P 20010405

AN 2003-058524 [05] WPIDS

AB WO 200281643 A UPAB: 20030121

NOVELTY - Preparing a **library** of **polynucleotides** comprises contacting a parent set of polynucleotides with at least 1 class IIS restriction enzyme to form polynucleotide fragments. Members of the members of the set of polynucleotides comprise at least 1 common class IIS restriction site capable of being cleaved by the at least 1 IIS restriction enzymes.

DETAILED DESCRIPTION - Preparing a **library** of **polynucleotides** comprises:

(a) contacting a parent set of polynucleotides with at least 1 class IIS restriction enzyme to form polynucleotide fragments (members of the members of the set of polynucleotides comprise at least 1 common class IIS restriction site capable of being cleaved by at least 1 IIS restriction enzymes);

(b) inactivating at least 1 class IIS restriction enzymes or separating the at least 1 class IIS restriction enzyme from the fragments; and

(c) ligating the fragments to yield full-length polynucleotides while allowing for the interchange of analogous fragments, thus forming the **library** of **polynucleotides**.

INDEPENDENT CLAIMS are also included for:

(1) a **library** of **polynucleotides** prepared by the methods above;

(2) a method of preparing a polynucleotide with a predetermined property; and

(3) a method of preparing a polynucleotide.

USE - The method is useful for preparing a **library** of **polynucleotides** by directed fragmentation of polynucleotides combined with fragment interchange or ligation. This is also useful for generating large cDNA libraries.

ADVANTAGE - As compared to the prior art, the method allows less **random** recombination, avoids the use of polymerase or **PCR** (**polymerase chain reaction**) for assembly of shuffled genes and can be applied readily to RNA molecules.

Dwg.0/1

L21 ANSWER 24 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-643398 [69] WPIDS

DOC. NO. CPI: C2004-014241

TITLE: Identifying regulator polypeptides which influence target transcriptional regulatory regions, useful for treating cancer, comprises introducing host cells expressing the polypeptide into a **library** of **polynucleotides**.

DERWENT CLASS: B04 D16

Search completed by David Schreiber 308-4292

INVENTOR(S): SMITH, E S; ZAUDERER, M
PATENT ASSIGNEE(S): (UYRP) UNIV ROCHESTER
COUNTRY COUNT: 100
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002062822	A2	20020815	(200269)*	EN	224
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW					
US 2002192675	A1	20021219	(200303)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002062822	A2	WO 2002-US2814	20020204
US 2002192675	A1 Provisional	US 2001-265589P	20010202
	Provisional	US 2001-265880P	20010205
	Provisional	US 2001-271423P	20010227
		US 2002-61395	20020204

PRIORITY APPLN. INFO: US 2001-271423P 20010227; US 2001-265589P 20010202; US 2001-265880P 20010205; US 2002-61395 20020204

AN 2002-643398 [69] WPIDS

AB WO 200262822 A UPAB: 20040115

NOVELTY - Identifying polynucleotides encoding a regulator polypeptide, whose expression induces activation of a target transcriptional regulatory region in a host cell, comprising providing a population of eukaryotic host cells capable of expressing the polypeptide, introducing into the host cell a **library** of **polynucleotides** encoding the polypeptides, permitting expression of the polypeptides, and recovering them from the host cells, is new.

DETAILED DESCRIPTION - Identifying polynucleotides encoding a regulator polypeptide, whose expression induces activation of a target transcriptional regulatory region in a host cell, comprising:

(a) providing a population of eukaryotic host cells capable of expressing the regulator polypeptide, where the host cells comprise a target transcriptional regulatory region which is naturally induced in a target cellular process, where the target transcriptional regulatory region is operably associated with a polynucleotide encoding a gene product, the expression of which results in host cell death or cause the host cells to exhibit pre-determined modified phenotype, and where the gene product is expressed upon activation of target transcriptional regulatory region;

(b) introducing into the population of host cells a **library** of **polynucleotides** constructed in a poxvirus vector, encoding, through operable association with a vector or the poxvirus transcriptional regulatory region, candidate regulator polypeptides, each candidate regulator polypeptide comprising:

(i) a candidate peptide; and

(ii) a molecular scaffold fused to the peptide so that the peptide is

displayed on the surface of the candidate regulator polypeptide;

(c) permitting expression of the plurality of candidate regulator polypeptides in the host cells under conditions where host cell death or the modified phenotype can be detected; and

(d) recovering **polynucleotides** of the **library** from those individual host cells which undergo cell death, or the poxvirus vector particles comprising the polynucleotides from the host cells which exhibit or failed to exhibit the modified phenotype.

INDEPENDENT CLAIMS are also included for the following:

(1) a kit for the identification of the regulator polypeptide, comprising a **library** of the novel **polynucleotides** and a population of eukaryotic host cells, where the polynucleotides encoding the polypeptides are recoverable from individual host cells which undergo cell death or which exhibit or failed to exhibit the modified phenotype;

(2) an isolated polynucleotide which encodes a regulator polypeptide, produced by the novel method; and

(3) a composition comprising the regulator polypeptide and a carrier.

ACTIVITY - Cytostatic; Antiarrhythmic; Cardiant; Vasotropic; Anorectic; Neuroprotective; Osteopathic; Antipsoriatic; Antibacterial; Virucide; Anti-HIV (human immunodeficiency virus); Vulnerary.

No biological data is given.

MECHANISM OF ACTION - Gene therapy.

USE - The methods are useful in selecting and/or screening regulator molecules, such as polypeptides, which directly or indirectly induce or suppress the transcriptional activation of a target transcriptional regulatory region in a eukaryotic host cell. These regulator molecules may be used in preventing or treating cancers (e.g. breast or ovarian cancer), cardiovascular diseases (e.g. arrhythmia, heart failure, ischemia), obesity, neurodegenerative diseases (e.g. Alzheimer's disease), bone pathologies, dermatologic diseases (e.g. psoriasis), infections (e.g viral, bacterial), acquired immunodeficiency syndrome (AIDS), in cosmetic applications, and in wound healing. The method is also useful in screening regulator molecules that block antibiotic transport mechanisms, in drug toxicities and drug resistance applications, and in improving the performance of existing or developmental drugs. It may also be used in immunobiology, inflammation, allergic response, and in biotechnology applications.

Dwg.0/5

L21 ANSWER 25 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-519672 [55] WPIDS
CROSS REFERENCE: 2000-638570 [61]; 2001-607700 [69]
DOC. NO. CPI: C2002-147068
TITLE: Identifying cleavage sites of a target RNA, by adding target RNA to library of nucleic acids e.g. ribozyme, which comprise catalytic core **flanked** by **random** nucleotides and isolating nucleic acid that cleave target RNA.
DERWENT CLASS: B04 D16
INVENTOR(S): CLAWSON, G; PAN, W
PATENT ASSIGNEE(S): (UYPE-N) UNIV PENNSYLVANIA STATE; (PENN-N) PENN STATE RES FOUND
COUNTRY COUNT: 100
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002046449	A2	20020613	(200255)*	EN	79

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ

Search completed by David Schreiber 308-4292

core, where the **random** nucleotide regions are **flanked** on each side by **fixed** sequences which allow **amplification**. The target RNA is contacted with the library of Dzs in the absence of Mg2+, and Dzs that bind to the target RNA are separated from Dzs that do not bind to the target RNA using a non-denaturing polyacrylamide gel. An enriched library of Dzs is generated by **amplifying** by **PCR** Dzs using two **amplification primers**, followed by unidirectional **PCR amplification** using a single **primer** to generate single stranded Dzs. The method further involves steps generating, contacting and separating steps as above.

Cleavage sites in target RNA which are accessible to ASO are identified by generating a library of ASOs, where each ASO comprises regions of **random** nucleotides **flanked** by **fixed** sequences which allow reamplification and transcription. Target RNA is contacted with the library of ASOs, ASOs that bind to the target RNA are separated, and an enriched **library** of antisense **oligonucleotides** is generated. The steps are repeated least four times to obtain selected ASOs, which are sequenced and the sequences compared with the sequence of the target RNA.

An INDEPENDENT CLAIM is also included for a catalytically active Rz, ASO and Dz produced by (M).

USE - (M) is useful for identifying one or more cleavage sites in a target RNA which are accessible to a Rz, Dz, or ASO, which is useful for making a catalytically active Rz, Dz or ASO, that is specific for a target RNA and accessible to a cleavage site on the target RNA, by identifying a cleavage site on a target RNA by (M), and constructing a Rz, Dz or ASO comprising a sequence that is complementary to the cleavage site. An ASO made by the process is useful for conducting real-time **PCR**, and an assay with a **fixed** polynucleotide array, by labeling the ASO with a detectable label to generate a labeled probe and using the labeled probe (claimed). The target RNA is isolated from any source, including eukaryotic and prokaryotic RNA, RNA from plants, mammals, fungi and various pathogenic organisms such as bacteria and viruses including hepatitis B virus, hepatitis C virus (HCV), human immunodeficiency virus (HIV) and human papillomavirus (HPV).

ADVANTAGE - (M) allows the rapid determination of accessible target sites throughout relatively long target RNAs.

Dwg.0/13

L21 ANSWER 26 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-490079 [52] WPIDS
DOC. NO. CPI: C2002-139160
TITLE: Producing recombinant polynucleotides useful in biochemical studies, comprises conducting a polymerization with multi-cyclic extension reactions with unidirectional single-stranded polynucleotide fragments as templates.
DERWENT CLASS: B04 D16
INVENTOR(S): JUN, Y J; JUNG, G H; LEE, G U; LEE, S H; RYU, E J; SHIN, Y C; JEON, Y; JUNG, K; LEE, K; LEE, S; RYU, E; SHIN, Y; JEON, Y J; JUNG, K H; LEE, K W
PATENT ASSIGNEE(S): (AMIC-N) AMICOGEN INC; (AMIC-N) AMICOGEN CO LTD; (JEON-I) JEON Y; (JUNG-I) JUNG K; (LEEK-I) LEE K; (LEES-I) LEE S; (RYUE-I) RYU E; (SHIN-I) SHIN Y
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

(1) polynucleotides, where the relative abundance of at least one target polynucleotide has been reduced relative to a non-target polynucleotide, and where at least one target polynucleotide is any one of the 16 genes listed in the specification;

(2) a kit for the enrichment of at least one low abundance polynucleotide in a sample of polynucleotides, where the sample comprises at least one high abundance polynucleotide and at least one low abundance polynucleotide, and where the kit comprises at least one enzymatically non-extendable nucleobase oligomer having a nucleobase sequence complementary to the high abundance target polynucleotide;

(3) analyzing gene expression in a sample having at least one high abundance polynucleotide;

(4) synthesizing a cDNA library enriched for at least one low abundance polynucleotide; and

(5) enriching a sample for one or more low abundance polynucleotides.

USE - The methods are useful for the selective enrichment of low abundance polynucleotides in a sample. The enriched low abundance polynucleotides can be used in analyzing gene expression in a sample and creating cDNA libraries.

Dwg.0/17

L21 ANSWER 3 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1

ACCESSION NUMBER: 2003:951225 HCAPLUS
DOCUMENT NUMBER: 140:24086
TITLE: Methods and hemi-**random** **oligonucleotides** probes for generating directed sequence **libraries**
INVENTOR(S): Kazakov, Sergei A.; Vlassov, Alexander V.; Johnston, Brian H.
PATENT ASSIGNEE(S): Somagenics, Inc., USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003100100	A1	20031204	WO 2003-US16662	20030527

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2002-383208P P 20020524

AB The invention provides methods and reagents useful for preparation of directed sequence libraries. Methods of the invention include the use of hemi-**random** oligonucleotide probes containing both defined and **random** sequences. Sequences selected from **random** libraries that hybridize to adjacent positions on a polynucleotide target are ligated and amplified, representing a directed library of sequences that correspond to sequences of the target. Masking oligonucleotides that

hybridize with the defined sequences are included to prevent parasitic ligation of the probes and to promote target-dependent ligation of sequences that are complementary to target sequences.

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 4 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:435185 HCAPLUS
DOCUMENT NUMBER: 139:18313
TITLE: Directed shuffling of nucleic acids using templates to direct recombination and size-insensitive **primer** independent **amplification**
INVENTOR(S): Dupret, Daniel; Masson, Jean Michel; Lefevre, Fabrice
PATENT ASSIGNEE(S): Proteus S.A., Fr.
SOURCE: U.S. Pat. Appl. Publ., 32 pp., Cont.-in-part of U.S. Ser. No. 840,861.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003104417	A1	20030605	US 2002-131175	20020425
FR 2782323	A1	20000218	FR 1998-10338	19980812
FR 2782323	B1	20020111		
WO 2000009679	A1	20000224	WO 1999-FR1973	19990811
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002160366	A1	20021031	US 2001-840861	20010425
US 2003215800	A9	20031120		

PRIORITY APPLN. INFO.:

FR 1998-10338	A	19980812
WO 1999-FR1973	A	19990811
US 2000-723316	A2	20001128
US 2001-285998P	P	20010425
US 2001-840861	A2	20010425
WO 2002-FR1435	A	20020425

AB A method of gene shuffling that uses templates to direct ligation of **randomly** generated DNA fragments followed by ligation and **primer**-independent **amplification** is described. The method does not require size fractionation or preliminary **amplification** of DNA and is more efficient in generating recombinants than prior art methods. The use of templates to assemble sequences can protect preferred regions, such as the region encoding an active site, from modification. **Random** DNA fragments are generated, e.g. by limited digestion with DNAse I, denatured, and hybridized to a template DNA. The hybridization products are then treated to create novel polynucleotides. This may be by simple ligation; gap filling and ligation, or overlap removal with a FLAP endonuclease and ligation. Recombinants are then cloned into a suitable host for phenotypic screening.

L21 ANSWER 5 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:376269 HCAPLUS
DOCUMENT NUMBER: 138:380368
TITLE: Shuffling polynucleotides using assembly templates without polynucleotide extension reaction
INVENTOR(S): Dupret, Daniel; Lefevre, Fabrice; Masson, Jean Michel
PATENT ASSIGNEE(S): Fr.
SOURCE: U.S. Pat. Appl. Publ., 36 pp., Cont.-in-part of U.S. Ser. No. 840,861.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2003092023	A1	20030515	US 2002-153706	20020524
FR 2782323	A1	20000218	FR 1998-10338	19980812
FR 2782323	B1	20020111		
WO 2000009679	A1	20000224	WO 1999-FR1973	19990811
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 2002160366	A1	20021031	US 2001-840861	20010425
US 2003215800	A9	20031120		

PRIORITY APPLN. INFO.:

FR 1998-10338	A	19980812
WO 1999-FR1973	A	19990811
US 2000-723316	A2	20001128
US 2001-285998P	P	20010425
US 2001-840861	A2	20010425

AB A method of gene shuffling is provided using hybridization of fragments on assembly templates, wherein the fragments are not themselves the templates. At least two homologous polynucleotide fragments are hybridized to one or more assembly templates to form at least one recombinant polynucleotide, wherein the fragments are shorter than all or substantially all of the assembly templates. No polymerization or extension is used to create a sequence complementary to the template or to fill in long gaps, and the fragments are non-initiating fragments that do not act as extension primers. The formation of the recombinant polynucleotide entails ligating nicks and, where necessary, any one of or any combination of gap-filling techniques. The invention is particularly aimed at generating novel polynucleotides that differ in some advantageous respect compared to a reference sequence. Further, the invention includes reaction mixts. created by or during the method, sequences created by the method, hosts and vectors containing same, and proteins translated therefrom. Advantages of the invention include: (1) control over the locations of recombination; (2) generation of more recombination and incorporation of fragments per reaction cycle; (3) increased efficiency by generating relatively few unshuffled parental clones and duplicate chimeras; and (4) little preparation of the starting DNA library. The method is exemplified with a starting library of 10 gene mutants of ponB coding for

penicillin-binding protein 1b of Escherichia coli, and xylanase genes from Thermotoga neapolitana or Acidobacterium capsulatum.

L21 ANSWER 6 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2003-689675 [65] WPIDS
DOC. NO. NON-CPI: N2003-550996
DOC. NO. CPI: C2003-189158
TITLE: New signaling DNA construct with an enzymatic DNA sequence and a DNA chain of ribonucleotide linkage, useful for isolating nucleic acid enzymes possessing desired characteristics, and designing a signaling allosteric deoxyribozyme.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): BRENNAN, J; LI, Y; LIU, Z; MEI, S
PATENT ASSIGNEE(S): (UYMC-N) UNIV MCMASTER
COUNTRY COUNT: 102
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003068963	A1	20030821	(200365)*	EN	65

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT SD SE SI SK SL SZ TR TZ UG ZM ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SC SD SE SG SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003068963	A1	WO 2003-CA198	20030211

PRIORITY APPLN. INFO: US 2002-431229P 20021206; US 2002-356727P 20020215; US 2002-402556P 20020812
AN 2003-689675 [65] WPIDS
AB WO2003068963 A UPAB: 20031009
NOVELTY - A signaling DNA construct (I) comprising an enzymatic DNA sequence, and a DNA chain having a ribonucleotide linkage **flanked** by a fluorophore modified oligonucleotide and a quencher modified oligonucleotide in sufficient proximity to each other where, in the absence of catalysis, fluorescence from the fluorophore is quenched by the quencher, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for:

(1) selection of an enzymatic DNA sequence, comprising inserting a **random** sequence into a DNA chain having a ribonucleotide linkage by a fluorophore modified oligonucleotide and a quencher modified oligonucleotide and determining whether a fluorescent signal is generated where the fluorophore modified oligonucleotide and the quencher modified oligonucleotide in sufficient proximity to each other where, in the absence of catalysis, fluorescence from the fluorophore is quenched by the quencher;

(2) detection of an enzymatic DNA sequence, comprising providing a **library** of **oligonucleotide** to be screened, ligating the oligonucleotides to an acceptor sequence comprising a ribonucleotide linkage **flanked** by a fluorophore modified oligonucleotide and a

quencher modified oligonucleotide, and determining whether a fluorescent signal is generated due to cleavage at the ribonucleotide linkage;

(3) selection of a DNA enzyme, comprising providing a **library** of **oligonucleotide** to be screened, ligating the oligonucleotides to an acceptor sequence comprising a ribonucleotide linkage **flanked** by a fluorophore modified oligonucleotide and a quencher modified oligonucleotide, and determining whether a fluorescent signal is generated due to cleavage at the ribonucleotide linkage, and amplifying sequences which generate a fluorescent signal;

(4) selection of an aptamer sequence, comprising conjugating a **library** of **oligonucleotide** sequences to (I) to provide a conjugate molecule, incubating the conjugate molecule in the presence of a desired target, determining whether a fluorescent signal is generated, and amplifying sequences which generate a signal;

(5) a kit for the selection of an enzymatic DNA sequence, comprising a DNA chain having a site for insertion of test nucleotide sequence, and a ribonucleotide linkage **flanked** by a fluorophore modified oligonucleotide and a quencher modified oligonucleotide in sufficient proximity to each other where, in the absence of catalysis, fluorescence from the fluorophore is quenched by the quencher and in the presence of a catalytic test nucleotide sequence, a fluorescent signal is generated; and

(6) detection of a co-factor, comprising providing (I), introducing a sample, and determining whether a signal is generated, where, in the presence of a required co-factor, cleavage occurs at the ribonucleotide linkage and a fluorescence signal is generated.

USE - The methods and compositions are useful for detecting and isolating nucleic acid enzymes which possess desired characteristics, designing a signaling allosteric deoxyribozyme, and for solution-based assays for detecting specific analytes.

Dwg.0/8

L21 ANSWER 7 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2003-627409 [59] WPIDS
DOC. NO. CPI: C2003-171486
TITLE: New engineered binding proteins derived from chaperonin or rubredoxin, useful for selecting and screening for members that have binding affinity to compounds of interest.
DERWENT CLASS: B04 D16
INVENTOR(S): NOCK, S; WILSON, D S
PATENT ASSIGNEE(S): (NOCK-I) NOCK S; (WILS-I) WILSON D S; (ZYOM-N) ZYOMYX INC
COUNTRY COUNT: 102
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003061570	A2	20030731	(200359)*	EN	153
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS LU MC MW MZ NL OA PT SD SE SI SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SC SD SE SG SK SL TJ TM TN TR TT TZ UA UG UZ VC VN YU ZA ZM ZW					
US 2004009530	A1	20040115	(200406)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE

WO 2003061570 A2		WO 2003-US1362	20030116
US 2004009530 A1	Provisional	US 2002-349804P	20020116
	Provisional	US 2002-349999P	20020117
		US 2003-347542	20030116

PRIORITY APPLN. INFO: US 2002-349999P 20020117; US 2002-349804P 20020116; US 2003-347542 20030116

AN 2003-627409 [59] WPIDS

AB WO2003061570 A UPAB: 20030915

NOVELTY - An engineered protein, is new.

DETAILED DESCRIPTION - The parent protein that corresponds to the engineered protein comprises a three-layer swiveling beta / beta / alpha domain. The central beta sheet of the domain is parallel and the other beta sheet is antiparallel. At least one portion of the primary sequence of the engineered protein is determined by an operation of an engineering scheme on the primary sequence of the parent protein, with the proviso that the portion of the primary sequence of the protein that is determined by the operation comprises at least 5% or does not exceed 50% of the length of the primary sequence of the protein. INDEPENDENT CLAIMS are also included for:

(1) a composition comprising the above engineered protein and a carrier;

(2) a nucleic acid encoding the above engineered protein or a mutated chaperonin or rubredoxin protein;

(3) an array comprising a plurality of the above engineered proteins immobilized on a solid support;

(4) determining whether the above engineered protein binds to a compound;

(5) using the engineered protein;

(6) detecting a compound in a sample;

(7) a mutated chaperonin or rubredoxin protein, where one or more portions of the mutated chaperonin or rubredoxin polypeptide vary by engineering of at least 10 amino acids from the corresponding portion of the wild-type chaperonin substrate-binding domain or wild-type rubredoxin sequence and where the sequence of the mutated chaperonin or rubredoxin protein has at least 50% total amino acid sequence identity with the wild-type chaperonin substrate-binding domain or wild-type rubredoxin sequence;

(8) an expression vector comprising the above nucleic acid or an expression cassette operably linked to the above nucleic acid molecule;

(9) a host cell comprising the nucleic acid molecule or expression vector;

(10) making an engineered protein or preparing an engineered chaperonin binding domain library or rubredoxin **library** from a set of paired **oligonucleotides**, where the first oligonucleotide in each pair includes a region that is complementary to the corresponding second oligonucleotide in each pair, and where at least one oligonucleotide in the set includes a **randomized** sequence; and

(11) a library of proteins comprising a plurality of engineered proteins cited above.

USE - The engineered protein is useful in selecting and screening for members that have binding affinity to compounds of interest.

Dwg.0/26

L21 ANSWER 8 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2003-513977 [48] WPIDS
DOC. NO. CPI: C2003-137696

Wilder 09/869,891

TITLE: New apparatus with a substrate and a modified nucleotide aptamer for monitoring biological interactions, useful for diagnosing and treating NF-kB aptamer-related diseases, such as toxic shock, rheumatoid arthritis, cancer and AIDS.

DERWENT CLASS: B04 D16

INVENTOR(S): GORENSTEIN, D G; HERZOG, N; LUXON, B A; YANG, X B; GORENSTEIN, D

PATENT ASSIGNEE(S): (GORE-I) GORENSTEIN D G; (HERZ-I) HERZOG N; (LUXO-I) LUXON B A; (YANG-I) YANG X B; (TEXA) UNIV TEXAS SYSTEM

COUNTRY COUNT: 97

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003050290	A2	20030619	(200348)*	EN	67
RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW					
US 2003162190	A1	20030828	(200357)		
AU 2002363923	A1	20030623	(200420)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003050290	A2	WO 2002-US25049	20020807
US 2003162190	A1 Provisional	US 2001-334887P	20011115
		US 2002-214417	20020806
AU 2002363923	A1	AU 2002-363923	20020807

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2002363923	A1 Based on	WO 2003050290

PRIORITY APPLN. INFO: US 2001-334887P 20011115; US 2002-214417 20020806

AN 2003-513977 [48] WPIDS

AB WO2003050290 A UPAB: 20030729

NOVELTY - An apparatus for monitoring biological interaction comprises a substrate and a modified aptamer attached to the substrate, where a target molecule or its portion, contacted with the modified aptamer under conditions to allow complexation between the modified aptamer and the target molecule or its portion, is detected.

DETAILED DESCRIPTION - Apparatus or monitoring biological interaction alternatively comprises a substrate, a modified nucleotide aptamer attached to the substrate having a desired binding efficiency for a target protein or its portion, and a detection system that identifies complexes of a target protein or its portion to the modified nucleotide aptamer, or a nucleic acid binding protein attached to the substrate, where the nucleic acid binding protein comprises a protein or its portion having a desired binding efficiency for a target modified aptamer or its portion.

INDEPENDENT CLAIMS are also included for the following:

(1) a process for monitoring biological interactions comprising

attaching a modified nucleotide aptamer that specifically binds to a target molecule or its portion to a substrate, complexing the modified nucleotide aptamer with a target molecule or its portion, and detecting interactions between the aptamer and target molecule;

(2) an aptamer selected to bind nuclear factor NF-kB or its constituents essentially homologous to nucleotide sequence S1, (S1) GGG GTG NTG TXX XGN GXN XNC,

where

X = G or C;

N = G, C, A or T

and where at least one nucleotide is an achiral thiophosphate or a dithiophosphate with a Kd of up to 50 nM;and

(3) a device comprising a substrate and one or more aptamers that bind to the substrate, where one or more aptamers are essentially homologous to the sequence of oligonucleotides with any of 135 fully defined sequence of 15-49 base pairs (bp), given in the specification.

ACTIVITY - Antibacterial; Immunosuppressive; Antirheumatic; Antiarthritic; Antiinflammatory; Cytostatic; Anti-HIV; Antiarteriosclerotic; Virucide; Neuroprotective. No biological data given.

MECHANISM OF ACTION - Phosphorothioate-Agonist; Phosphorothioate-Antagonist.

USE - The methods and apparatus of the present invention are useful for monitoring biological interactions and in functional proteomics. The NF-kB aptamers can also be used in diagnosing and treating NF-kB aptamer-related diseases, such as toxic shock, sepsis, rheumatoid arthritis, Crohn's disease, generalized inflammatory bowel disease, asbestos lung diseases, Hodgkin's disease, prostate cancer, ventilator induced lung injury, general cancer, AIDS, human cutaneous T cell lymphoma, lymphoid malignancies, HTLV-1 induced adult T-cell leukemia, atherosclerosis, cytomegalovirus, herpes simplex virus, JCV, SV-40, rhinovirus, influenza, neurological disorders and lymphomas.

Dwg.0/12

L21 ANSWER 9 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-229645 [22] WPIDS

CROSS REFERENCE: 2003-248055 [24]; 2003-248080 [24]

DOC. NO. CPI: C2003-059185

TITLE: Preparing a **variant** polynucleotide having a desired property, comprises using a reassembly process of preferably blunt-ended restriction enzyme fragments prepared from a starting population of heterologous polynucleotides.

DERWENT CLASS: B04 D16

INVENTOR(S): BOVENBERG, R A L; KERKMAN, R

PATENT ASSIGNEE(S): (STAM) DSM NV

COUNTRY COUNT: 100

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003010311	A2	20030206	(200322)*	EN	18

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW

Wilder 09/869,891

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003010311 A2		WO 2002-EP8222	20020723

PRIORITY APPLN. INFO: EP 2001-203458 20010911; EP 2001-202822 20010723

AN 2003-229645 [22] WPIDS

CR 2003-248055 [24]; 2003-248080 [24]

AB WO2003010311 A UPAB: 20030410

NOVELTY - Preparing a **variant** polynucleotide having a desired property comprises using a reassembly process of preferably blunt-ended restriction enzyme fragments prepared from a starting population of heterologous polynucleotides in the presence of a ligase.

DETAILED DESCRIPTION - Preparing a **variant** polynucleotide having a desired property comprises subjecting a population of polynucleotides to separate digestions with a restriction enzyme, preferably capable of generating blunt-ended fragments, combining the digests, applying one or more cycles of denaturation, annealing and reassembly in the presence of a ligase, optionally **amplifying** the reassembled **polynucleotides**, preparing a **library** of the resulting **variant polynucleotides**, and screening the **library** of **variant polynucleotides** for a **variant** polynucleotide with a desired property.

INDEPENDENT CLAIMS are included for:

(a) a process for producing a **variant** polypeptide comprising expressing the **variant** polynucleotide prepared by the process cited above in a suitable host, and optionally recovering the produced polypeptide; and

(b) a process for producing a primary or secondary metabolite comprising expressing the **variant** polynucleotide prepared by the process cited above in a suitable host, and optionally recovering the produced metabolite.

USE - The methods are useful for preparing **variant** polynucleotides used for producing **variant** polypeptides or metabolites.

ADVANTAGE - The present method enables the **random** combination of mutated positions in a rapid, reproducible and highly controllable way. The recombination frequency is high and the chance to re-isolate the starting polynucleotide is low.

Dwg.0/4

L21 ANSWER 10 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2003-248055 [24] WPIDS

CROSS REFERENCE: 2003-229645 [22]; 2003-248080 [24]

DOC. NO. CPI: C2003-063915

TITLE: Preparing a **variant** polynucleotide having a desired property comprises subjecting a population of polynucleotides to two or more separate PCRs comprising forward or reverse mutation-specific and reverse **primers**.

DERWENT CLASS: B04 D16

INVENTOR(S): BOVENBERG, R A L; KERKMAN, R

PATENT ASSIGNEE(S): (STAM) DSM NV

COUNTRY COUNT: 100

PATENT INFORMATION:

Search completed by David Schreiber 308-4292

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2003010183	A2	20030206	(200324)*	EN	20

RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SK SL SZ TR TZ UG ZM ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2003010183	A2	WO 2002-EP8225	20020723

PRIORITY APPLN. INFO: EP 2001-203457 20010911; EP 2001-202821 20010723

AN 2003-248055 [24] WPIDS

CR 2003-229645 [22]; 2003-248080 [24]

AB WO2003010183 A UPAB: 20030410

NOVELTY - Preparing a **variant** polynucleotide with a desired property comprising subjecting a population of polynucleotides to two or more separate PCRs, a first **PCR** with a forward mutation-specific **primer** for a position to be mutated and a reverse universal **primer**, a second **PCR** with a forward universal **primer** and a reverse mutation-specific **primer** for a position to be mutated, and a third or more **PCR** with a suitable forward and reverse **primer**, is new.

DETAILED DESCRIPTION - Preparing a **variant** polynucleotide with a desired property comprising subjecting a population of polynucleotides to two or more separate PCRs, a first **PCR** with a forward mutation-specific **primer** for a position to be mutated and a reverse universal **primer**, a second **PCR** with a forward universal **primer** and a reverse mutation-specific **primer** for a position to be mutated, and a third or more **PCR** with a suitable forward and reverse **primer**, is new.

The method comprises:

(a) subjecting a population of polynucleotides to two or more separate PCRs, a first **PCR** with a forward mutation-specific **primer** for a position to be mutated and a reverse universal **primer**, a second **PCR** with a forward universal **primer** and a reverse mutation-specific **primer** for a position to be mutated, and a third or more **PCR** with a suitable forward and reverse **primer**;

(b) assembling the products of the two or more PCRs by a polymerase;

(c) optionally, **amplifying** the assembled polynucleotides;

(d) preparing a **library** of the resulting **variant polynucleotides**; and

(e) screening the **library** of **variant polynucleotides** for a **variant** polynucleotide with a desired property.

INDEPENDENT CLAIMS are also included for:

(1) producing a **variant** polypeptide by expressing the **variant** polynucleotide prepared in the above method in a suitable host, and optionally, recovering the produced polypeptide; and

(2) producing a primary or secondary metabolite by expressing the **variant** polynucleotide prepared in the above method, and optionally recovering the produced metabolite.

USE - The methods are useful for preparing **variant** polynucleotides, polypeptides and primary or secondary metabolites (claimed).

ADVANTAGE - The methods of the invention advantageously enable the mutagenesis of a polynucleotide and the **random** combination of mutated positions to be performed in one process, without the necessity for prior fragmentation of the polynucleotide.

Dwg.0/3

L21 ANSWER 11 OF 89 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 2003342497 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12874379
TITLE: User-friendly algorithms for estimating completeness and diversity in **randomized** protein-encoding libraries.
AUTHOR: Patrick Wayne M; Firth Andrew E; Blackburn Jonathan M
CORPORATE SOURCE: Department of Biochemistry, University of Cambridge, Tennis Court Road, Cambridge CB2 1GA, UK.
SOURCE: Protein engineering, (2003 Jun) 16 (6) 451-7.
~~Journal code:~~ 8801484. ISSN: 0269-2139.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200403
ENTRY DATE: Entered STN: 20030723
Last Updated on STN: 20040312
Entered Medline: 20040311

AB Directed evolution of proteins depends on the production of molecular diversity by **random** mutagenesis. While a number of methods have been developed for introducing this diversity, the best ways to sample it are not always clear. Here we used simple statistics to analyse completeness and diversity in **randomized libraries** generated by **oligonucleotide**-directed mutagenesis, error-prone **polymerase chain reaction** (epPCR) and in vitro recombination of highly homologous sequences. For oligonucleotide-directed mutagenesis, we derive equations to estimate how complete a given library is expected to be and also to predict the size of library required to give a fixed probability of being 100% complete. We describe the statistical bases for computer programs which estimate the number of distinct variants represented in epPCR and shuffled libraries, dubbed PEDEL and DRIVeR, respectively. These programs allow the user to calculate (rather than guess) the diversity represented in a given library and also provide empirical guidelines for maximizing this diversity. PEDEL and DRIVeR are available at www.bio.cam.ac.uk/ approximately blackburn/stats.html.

L21 ANSWER 12 OF 89 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 2003277552 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12804117
TITLE: Identification and characterization of a consensus DNA binding element for the zinc finger transcription factor TIEG/EGRalpha.
AUTHOR: Chrisman Holly R; Tindall Donald J
CORPORATE SOURCE: Department of Urology Research, Mayo Clinic/Foundation, Rochester, Minnesota 55905, USA.

Search completed by David Schreiber 308-4292

SOURCE: DNA and cell biology, (2003 Mar) 22 (3) 187-99.
Journal code: 9004522. ISSN: 1044-5498.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200307
ENTRY DATE: Entered STN: 20030614
Last Updated on STN: 20030708
Entered Medline: 20030707

AB TGFbeta-Inducible Early Gene (TIEG) and the alternatively-transcribed Early Growth Response Gene alpha (EGRalpha) share a Cys(2)His(2) three-zinc finger region with high homology to Sp1 within its zinc finger region. Three-zinc finger transcription factors bind to GC-rich sequences, with small variations in consensus sequence between subfamilies. In this work, a consensus sequence was identified for TIEG/EGRalpha by expressing and purifying the zinc finger region of the protein, and using this to select a binding site from a **random oligonucleotide library** by iterative cycles of nitrocellulose filter binding and **PCR**. A fusion of the TIEG/EGRalpha with the VP16 activation domain supported transcription from this site when cloned in front of a heterologous promoter. Mutational analysis of the binding site identified a GT-rich core (5'-GGTGTG-3') that was necessary for binding, with mutations outside of this region causing only a small to moderate decrease in binding.

L21 ANSWER 13 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4

ACCESSION NUMBER: 2003:188733 BIOSIS
DOCUMENT NUMBER: PREV200300188733
TITLE: Design and applications of modified oligonucleotides.
AUTHOR(S): Gallo, M.; Montserrat, J. M.; Iribarren, A. M. [Reprint Author]
CORPORATE SOURCE: Laboratorio de Quimica de Acidos Nucleicos, Instituto de Investigaciones en Ingenieria Genetica y Biologia Molecular, CONICET-UBA, Vuelta de Obligado 2490, 2nd Piso, 1428, Buenos Aires, Argentina
airi@dna.uba.ar
SOURCE: Brazilian Journal of Medical and Biological Research, (February 2003) Vol. 36, No. 2, pp. 143-151. print.
CODEN: BJMRDK. ISSN: 0100-879X.
DOCUMENT TYPE: Article
General Review; (Literature Review)
LANGUAGE: English
ENTRY DATE: Entered STN: 16 Apr 2003
Last Updated on STN: 16 Apr 2003

AB Oligonucleotides have a wide range of applications in fields such as biotechnology, molecular biology, diagnosis and therapy. However, the spectrum of uses can be broadened by introducing chemical modifications into their structures. The most prolific field in the search for new oligonucleotide analogs is the antisense strategy, where chemical modifications confer appropriate characteristics such as hybridization, resistance to nucleases, cellular uptake, selectivity and, basically, good pharmacokinetic and pharmacodynamic properties. Combinatorial technology is another research area where oligonucleotides and their analogs are extensively employed. Aptamers, new catalytic ribozymes and deoxyribozymes are RNA or DNA molecules individualized from a **randomly** synthesized library on the basis of a particular property. They are identified by repeated cycles of selection and

amplification, using **PCR** technologies. Modified nucleotides can be introduced either during the amplification procedure or after selection.

L21 ANSWER 14 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2003:425381 HCAPLUS
DOCUMENT NUMBER: 139:96005
TITLE: **Random** oligonucleotide mutagenesis
AUTHOR(S): Sneeden, Jessica L.; Loeb, Lawrence A.
CORPORATE SOURCE: Department of Biochemistry, University of Washington, Seattle, WA, USA
SOURCE: Methods in Molecular Biology (Totowa, NJ, United States) (2003), 231(Directed Evolution Library Creation), 65-73
CODEN: MMBIED; ISSN: 1064-3745
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **Random** oligonucleotide mutagenesis is a method to generate diversity that consists of incorporating **random** mutations, encoded on a synthetic oligonucleotide, into a specific region of a gene. In this method, the oligonucleotides that encode a specific region of the protein of interest are synthesized which contain some determined degree of **randomization**. The result is a library of mutant protein sequences, each of which contains different mutations. These oligonucleotides are then amplified by minimal cycles of **PCR** to generate double stranded mols., and cloned by restriction digest into a plasmid-encoded wild-type enzyme, replacing the wild-type region of interest. This creates a library of plasmid-encoded mutant enzymes that can be transformed into an appropriate cell strain and subjected to selection for the desired phenotype. Procedures for the creation of a mutant **library** using **random oligonucleotide** mutagenesis are outlined.
REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 15 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 5
ACCESSION NUMBER: 2002:449421 HCAPLUS
DOCUMENT NUMBER: 137:28987
TITLE: Killer primer method and kit for construction of a rat liver low copy gene or cDNA library by normalization or **subtractive** hybridization using oligonucleotide probes
INVENTOR(S): Mugasimangalam, Raja C.
PATENT ASSIGNEE(S): QBI Enterprises, Ltd., India
SOURCE: PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002045472	A2	20020613	WO 2001-IB1343	20010711
WO 2002045472	A3	20030320		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS,

---

WO 2002038757 A1 20020516 (200252)* EN 84
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
AU 2001074635 A 20020521 (200260)
KR 2002036665 A 20020516 (200273)
US 2003152943 A1 20030814 (200355)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002038757	A1	WO 2001-KR1031	20010616
AU 2001074635	A	AU 2001-74635	20010616
KR 2002036665	A	KR 2001-41549	20010711
US 2003152943	A1	WO 2001-KR1031	20010616
		US 2002-148724	20020528

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001074635	A	Based on	WO 2002038757

PRIORITY APPLN. INFO: KR 2000-66889 20001110
AN 2002-490079 [52] WPIDS
AB WO 200238757 A UPAB: 20020815
NOVELTY - Producing (M1) recombinant polynucleotides (P) by conducting a polymerization process with multi-cyclic extension reactions, where the unidirectional single-stranded (P) fragments serve as templates and specific oligonucleotides are added to the reaction mixture as primers that are extended by template switching, is new.

DETAILED DESCRIPTION - Producing recombinant polynucleotides comprises:

(a) generating a pool of unidirectional single-stranded polynucleotide fragments **randomized** in length from at least one starting polynucleotide to be reassembled which have regions of similarity with each other;

(b) conducting a polymerization process with multi-cyclic extension reactions, where the unidirectional single-stranded polynucleotide fragments prepared by step (a) serve as templates, and specific oligonucleotides are added to the reaction mixture as primers which are extended by template switching, to produce at least one recombinant polynucleotide, and the resulting recombinant polynucleotides have different nucleotide sequences from the starting polynucleotides; and

(c) conducting a **polymerase chain reaction** (PCR) using at least one specific primer to amplify the recombinant polynucleotides prepared by step (b).

INDEPENDENT CLAIMS are also included for the following:

(1) constructing a recombinant DNA **library** comprising inserting the recombinant **polynucleotide** into a vector, and transforming an expression cell comprising the vector with the recombinant polynulceotide to obtain several clones; and

(2) evolving a polynucleotide towards a desired property comprising screening recombinant polynucleotides with a desired functional property

from the recombinant DNA library constructed by the method cited above.

USE - (M1) is useful for in vitro recombination of homologous polynucleotides and for producing a pool of recombinant DNA and a recombinant DNA library encoding mutant proteins, which allows the directed evolution of proteins by in vitro recombination. The method may also be used as a means for biochemical studies, as means for producing and screening a protein such as enzyme, antibody, vaccine, hormone, adsorption protein or plasma protein, which induces the change of substrate specificity, change of reaction specificity or change of safety of a protein, as well as can be applied in various industrial fields, e.g. development of medicine, improvement and enhancement of food quality, improvement of energy conversion rate, breeding and quality improvement in livestock and fishery, or development and production of novel chemical products. The method for constructing a recombinant DNA library may by used to screen a useful gene, or for identifying an improved mutant gene.

ADVANTAGE - The new method overcomes the problems of prior methods where a pool of various recombinant DNAs can be obtained more easily owing to the increased **randomness** introduced by a new principle different from prior art, and that **random** diversity of the polynucleotides is achieved in a short period of time.

Dwg.0/11

L21 ANSWER 27 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-435324 [46] WPIDS
DOC. NO. CPI: C2002-123631
TITLE: Novel oligonucleotide linker or population of linkers for preparing **polynucleotide libraries,** comprises an **oligonucleotide fixed** portion and an oligonucleotide **variable** portion.
DERWENT CLASS: B04 D16
INVENTOR(S): HAYASHIZAKI, Y
PATENT ASSIGNEE(S): (RIKE) RIKEN KK
COUNTRY COUNT: 23
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002028876	A2	20020411	(200246)*	EN	96
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR					
W: CA JP US					
EP 1325118	A2	20030709	(200345)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TR					

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002028876	A2	WO 2001-JP8805	20011005
EP 1325118	A2	EP 2001-974719	20011005
		WO 2001-JP8805	20011005

FILING DETAILS:

PATENT NO	KIND		PATENT NO
EP 1325118	A2	Based on	WO 2002028876

PRIORITY APPLN. INFO: JP 2000-306749 20001005

Search completed by David Schreiber 308-4292

AN 2002-435324 [46] WPIDS
AB WO 200228876 A UPAB: 20020722
NOVELTY - A linker (I) or a population of linkers comprising an oligonucleotide **fixed** portion and an oligonucleotide **variable** portion, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a double stranded linker or a population of linkers, comprising:

(a) a first oligonucleotide (ont1) single strand comprising an oligonucleotide single strand **fixed** portion and an oligonucleotide single strand **variable** portion; and

(b) a second oligonucleotide (ont2) single strand comprising an oligonucleotide single strand **fixed** portion annealed to he complementary oligonucleotide single strand **fixed** portion, so that the **variable** portion protrudes outside the double strand **fixed** portion of the linker;

(2) a population of linkers, comprising at least two (I);

(3) a linker-polynucleotide (II) or population of linker-polynucleotides comprising (I) or population of linkers and target first strand polynucleotide bound to the linker;

(4) a vector (II) comprising (II);

(5) preparing (I) or population of (I), by annealing ont1 to ont2, so that the **variable** portion protrudes outside the double strand **fixed** portion of the linker;

(6) binding a linker or population of linkers to mRNA, comprising treating mRNA with phosphatase and removing phosphate groups from uncapped mRNA, treating the product with pyrophosphatase, which removes the CAP structure from capped mRNA, and adding an RNA ligase in the presence of (I); and

(7) preparing a linker-polynucleotide, by treating mRNA by the method of (6), adding an RNA ligase in the presence of (I) or population of (I) and adding an oligo dT and synthesizing a polynucleotide complementary to the complete sequence of the mRNA.

USE - (I) is useful for binding a target single strand polynucleotide to a linker, by preparing (I) and annealing the **variable** portion of first strand of (I) to the target single strand polynucleotide and ligating the **fixed** portion of the second strand of the linker to the target. The method is useful for preparing a second strand polynucleotide, by synthesizing the second strand complementary to the first. (I) is also useful for preparing a linker-polynucleotide comprising a linker and a double-strand polynucleotide, by annealing the **variable** portion of the linker to the target, and synthesizing the second strand. Ligation is performed by a ligase in the presence of a ligase-stimulating agent, preferably polyethylene glycol. The linker and the target is DNA. The single or double strand polynucleotide is a long strand, full coding and/or full-length cDNA. The first strand cDNA is obtained from the Cap trapping at the 5' end of the mRNA. The cap-trapping cDNA is further normalized or **subtracted** before or after the ligation to linker. The method comprises increasing temperature to 65 deg. C before annealing the linker to the target and/or after synthesizing the second strand. The linker-polynucleotide is cleaved at both ends in restriction enzyme sites and inserted into a vector. (I) facilitates the preparation of a DNA/RNA hybrid, which comprises providing a full-length/coding or long polyA mRNAs, ligating and annealing the mRNA to (I), where the linker comprises a restriction enzyme site, annealing an oligo dT-**primer** comprising second restriction enzyme site to the mRNA, synthesizing a cDNA strand, isolating the hybrid by using restriction enzymes which recognize two specific restriction enzyme sites introduced, and cloning. (I) is further useful for marking a

polynucleotide library and distinguishing the **library**, where the **fixed** portion comprises a marker indicating a specific or defined tissue or species. (All claimed).

ADVANTAGE - The linkers facilitate the preparation of libraries more advantageously compared to conventional methods and in particular to the method of G-tailing. (I) does not require heavy metals and can be used at low temperature. The constant portion of (I) comprising a marker distinguishes and does not confuse libraries of different species.

Dwg.0/8

L21 ANSWER 28 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-179795 [23] WPIDS
DOC. NO. CPI: C2002-055904
TITLE: Forming **chimeric** polynucleotide by contacting single-stranded (ss) scaffold fragment, and donor fragment populations to form hybridized complex having ss regions which are filled-in, and ligating adjacent fragments.
DERWENT CLASS: B04 D16
INVENTOR(S): ARENSDORF, J J; COCO, W M; ENCELL, L P
PATENT ASSIGNEE(S): (ENCH-N) ENCHIRA BIOTECHNOLOGY CORP
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2002006469	A2	20020124	(200223)*	EN	65

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001073559 A 20020130 (200236)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2002006469	A2	WO 2001-US22640	20010718
AU 2001073559	A	AU 2001-73559	20010718

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001073559	A	Based on	WO 2002006469

PRIORITY APPLN. INFO: US 2000-692732 20001019; US 2000-218921P 20000718; US 2000-219085P 20000718; US 2000-691873 20001019

AN 2002-179795 [23] WPIDS

AB WO 200206469 A UPAB: 20020411

NOVELTY - Forming (M1) **chimeric** polynucleotide (I), comprising contacting a population of single-stranded (ss) scaffold fragments (SF) with population of donor fragments (DF) so that a complex (II) comprising at least one SF hybridized to two DFs at distal regions of SF, is formed, treating (II) so that ss regions of (II) are filled-in, and treating (II) so that adjacent fragments are ligated, is new.

Search completed by David Schreiber 308-4292

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) (I) prepared by (M1), and double-stranded (ds) (I) produced by (M1);

(2) a library (II) of (I) prepared by (M1);

(3) directed evolution by screening or selecting at least one ds (I) from library of ds (I), formed by (M1);

(4) preparing a population of SF, comprising:

(a) **amplifying** a oligonucleotide of interest in **PCR** , where 5' terminus of a first **primer** comprises 5' phosphate and 5' terminus of a second **primer** is devoid of 5' phosphate;

(b) contacting the **amplified** oligonucleotide with lambda exonuclease so that oligonucleotides having a 5' phosphate are digested, leaving ss oligonucleotides; and

(c) fragmenting ss oligonucleotides;

(5) a library of ds (I) formed by (M1); and

(6) a **chimeric** polynucleotide formed and selected by a directed evolution process involving (M1).

USE - (M1) is useful for a directed evolution process which involves forming a library of (I) by contacting first population of oligonucleotides (O1) with second population of oligonucleotides, to form a gapped homoduplex by hybridization, where the first and second populations of oligonucleotides are complementary to one another, treating gapped homoduplex with a polymerase where polynucleotide strand extension produces nicked polynucleotide, and treating the nicked polynucleotide with a ligase so that the nicks are ligated and screening the library of (I) for a characteristic of interest. The first and second population of oligonucleotides are derived from known polynucleotide of interest, and oligonucleotides of second population do not contain 5' phosphate groups and 3' hydroxyl groups. The method further involves repeating the steps using (I) as known polynucleotide of interest in subsequent round of directed evolution. The steps are repeated 2-50 times using a screened population of (I) as the parent polynucleotides used to generate SF and DF in a subsequent round of directed evolution. The method involves cloning the library of (I) into a vector prior to screening step which involves screening the function of transcribed and/or translated products of library of (I). The method further involves cloning (I) into expression vectors, transforming a cell line with the cloned **chimeric** polynucleotides, inducing expression of the cloned **chimeric** polynucleotide, assaying the expressed product for a characteristic of interest, and selecting the **chimeric** polynucleotide that expressed products with an improved characteristic of interest. transcribing and translating the **chimeric** polynucleotide in vitro, assaying the transcribed and translated products for a characteristic of interest, and selecting the **chimeric** polynucleotide that lead to transcribed and translated products with an improved characteristic of interest. (All claimed).

ADVANTAGE - The methods facilitate the generation of **chimeric** polynucleotides and do not require hybridizing donor fragments to a target- or full-length template. Because the **chimeragenesis** process does not rely upon a contiguous, full-length template, it is unnecessary to modify a template to facilitate its removal.

Dwg.0/6

L21 ANSWER 29 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2004-050991 [05] WPIDS
CROSS REFERENCE: 2000-303449 [26]; 2000-482862 [42]; 2000-491075 [43]; 2000-514667 [46]; 2001-300096 [31]; 2003-777161 [73]
DOC. NO. NON-CPI: N2004-041221

Search completed by David Schreiber 308-4292

Wilder 09/869,891

DOC. NO. CPI: C2004-020446
TITLE: Making recombinant nucleic acid designated Genetic Algorithm Guided Gene Synthesis is useful to generate encoded molecules with new or improved properties of industrial, agricultural and therapeutic importance.
DERWENT CLASS: B04 D16 S03 T01
INVENTOR(S): DEL CARDAYRE, S; GUSTAFSSON, C; MINSHULL, J; PATTEN, P A; SELIFONOV, S A; STEMMER, W P C; TOBIN, M
PATENT ASSIGNEE(S): (DCAR-I) DEL CARDAYRE S; (GUST-I) GUSTAFSSON C; (MINS-I) MINSHULL J; (PATT-I) PATTEN P A; (SELI-I) SELIFONOV S A; (STEM-I) STEMMER W P C; (TOBI-I) TOBIN M
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 2002183934	A1	20021205	(200405)*		53

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 2002183934	A1	Provisional	US 1999-116447P	19990119
		Provisional	US 1999-118854P	19990205
		CIP of	US 1999-416375	19991012
			US 2000-494282	20000118

PRIORITY APPLN. INFO: US 2000-494282 20000118; US 1999-116447P 19990119; US 1999-118854P 19990205; US 1999-416375 19991012
AN 2004-050991 [05] WPIDS
CR 2000-303449 [26]; 2000-482862 [42]; 2000-491075 [43]; 2000-514667 [46]; 2001-300096 [31]; 2003-777161 [73]
AB US2002183934 A UPAB: 20040120
NOVELTY - Making a recombinant nucleic acid by providing parental character strings (CS) corresponding to a number of nucleic acids, is new.

DETAILED DESCRIPTION - Making a recombinant nucleic acid by providing parental character strings (CS) corresponding to a number of nucleic acids, where the CS when aligned for maximum identity comprise at least one region of heterology, aligning the CS, defining a set of CS subsequences of at least two of the parental CS, providing a set of oligonucleotides corresponding to the subsequences, annealing the oligonucleotides, and elongating one or more oligonucleotides with a polymerase or ligase to produce one or more nucleic acids.

INDEPENDENT CLAIMS are also included for:

(a) making CS, comprising:

(a) providing a parental character string encoding a polynucleotide or polypeptide;

(b) providing a set of oligonucleotide CS of a pre-selected length that encode a number of single stranded oligonucleotide sequences comprising sequence fragments of the parental character string and their complement; and

(c) creating a set of derivatives of the parental sequence comprising sequence variant strings, where the set comprises a number of mutations, one per variant string;

(b) a library made by the above method further comprising synthesizing sets of single stranded oligonucleotides as described steps (b) and (c), and assembling a library of recombinant nucleic acids by

assembly **PCR** from the single stranded oligonucleotides;

(c) facilitating recombination between two or more divergent nucleic acids, comprising:

(a) aligning parental CS corresponding to the divergent nucleic acids to identify regions of sequence identity and regions of sequence diversity;

(b) defining a diplomat character string intermediate in sequence between parental CS;

(c) synthesizing at least a portion of the diplomat sequence to produce a diplomat nucleic acid; and

(d) recombining a mixture of selected nucleic acids comprising the parental nucleic acids or their fragments and the diplomatic nucleic acid;

(d) the mixture of nucleic acids produced by the above method;

(e) generating and recombining nucleic acids, comprising:

(a) inputting a number of amino acid sequence CS into a digital system;

(b) reverse translating the amino acid CS into a number of nucleic acid CS selected for species codon bias in a selected expression host and/or optimized sequence similarity between the nucleic acid CS; and

(c) synthesizing set(s) of oligonucleotides corresponding to one or more reverse translated nucleic a cid sequences;

(f) optimizing activity of a nucleic acid, comprising:

(a) prameterizing a set of nucleic acids or proteins to provide a set of multidimensional datapoints;

(b) extrapolating one or more postulated multidimensional datapoints from the set in (a); and

(c) converting the postulated multidimensional datapoint to a new character string corresponding to the postulated nucleic acid or protein;

(g) providing a library of recombinant nucleic acids which is enriched in a sequence of interest and selecting the library, comprising:

(a) producing an initial library of at least about 106 recombinant nucleic acids comprising at least about 105 different member types which are non-identical;

(b) hybridizing the library to population(s) of nucleic acids corresponding to subsequence(s) in the different library members;

(c) isolating members of the library which hybridize to the nucleic acid population(s), thereby enriching the library for members which hybridize to population(s) of nucleic acids; and

(d) selecting members of the enriched library for one or more properties of interest;

(h) the enriched library produced by the above method;

(i) generating a library of biological polymers, comprising generating a diverse population of CS in a computer by altering pre-existing CS and synthesizing the diverse population comprising the library of biological polymers;

(j) an integrated system comprising a compute having a first data set comprised of a first character string, a second data set comprised of a second character string, software for aligning the two CS, software for performing a genetic operation on one of the CS, an output file comprising a third data set comprised of a third character string having subsequences from the first two strings, and an oligonucleotide sequence output file comprising a number of overlapping oligonucleotide sequences corresponding to the third character string

USE - The invention is useful to generate encoded molecules with new or improved properties of industrial, agricultural and therapeutic importance.

Dwg.0/15

L21 ANSWER 30 OF 89 MEDLINE on STN DUPLICATE 6

Search completed by David Schreiber 308-4292

Wilder 09/869,891

ACCESSION NUMBER: 2002638588 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12398196
TITLE: Generation of amplifiable genome-specific **oligonucleotide** probes and **libraries**.
AUTHOR: Brukner Ivan; Tremblay Guy A; **Paquin Bruno**
CORPORATE SOURCE: Universite de Montreal, Quebec, Canada.. ibrukner@hotmail.com
SOURCE: BioTechniques, (2002 Oct) 33 (4) 874-6, 878, 880 passim. Journal code: 8306785. ISSN: 0736-6205.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200303
ENTRY DATE: Entered STN: 20021026
Last Updated on STN: 20030327
Entered Medline: 20030326

AB Here we describe a process for the generation of **oligonucleotide libraries** representative of a given nucleic acid. Starting from at **random** pool of DNA oligonucleotides, the technique selects only those that hybridize to the nucleic acid template. This selection yields a highly specific **library** that represents an **oligonucleotide** image of the chosen template. The novel quality of this approach is the generation of amplifiable oligonucleotide probes that are of unique length and are easily subjected to differential selection. Here we apply this technique to produce different genomic **oligonucleotide libraries** and show that these genomic **oligonucleotide libraries** do not cross-hybridize. Differential selection of these genomic **oligonucleotide libraries** produces **oligonucleotides** that can be used in the identification, characterzation, and isolation of nucleic acids.

L21 ANSWER 31 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 7
ACCESSION NUMBER: 2003:254721 HCAPLUS
DOCUMENT NUMBER: 138:249539
TITLE: Construction of a 'unigene' cDNA clone set by oligonucleotide fingerprinting allows access to 25,000 potential sugar beet genes
AUTHOR(S): Herwig, Ralf; Schulz, Britta; Weisshaar, Bernd; Hennig, Steffen; Steinfath, Matthias; Drungowski, Mario; Stahl, Dietmar; Wruck, Wasco; Menze, Andreas; O'Brien, John; Lehrach, Hans; Radelof, Uwe
CORPORATE SOURCE: Max-Planck Institute for Molecular Genetics, Berlin, D-14195, Germany
SOURCE: Plant Journal (2002), 32(5), 845-857 CODEN: PLJUED; ISSN: 0960-7412
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Access to the complete gene inventory of an organism is crucial to understanding physiol. processes like development, differentiation, pathogenesis, or adaptation to the environment. Transcripts from many active genes are present at low copy nos. Therefore, procedures that rely on **random** EST sequencing or on normalization and **subtraction** methods have to produce massively redundant data to get access to low-abundance genes. Here, we present an improved oligonucleotide fingerprinting (ofp) approach to the genome of sugar beet (Beta vulgaris), a plant for which practically no mol. information has been available. To identify distinct genes and to provide a

Search completed by David Schreiber 308-4292

representative 'unigene' cDNA set for sugar beet, 159,936 cDNA clones were processed utilizing large-scale, high-throughput data generation and anal. methods. Data anal. yielded 30,444 ofp clusters reflecting the number of different genes in the original cDNA sample. A sample of 10,961 cDNA clones, each representing a different cluster, were selected for sequencing. Standard sequence anal. confirmed that 89% of these EST sequences did represent different genes. These results indicate that the full set of 30,444 ofp clusters represent up to 25,000 genes. Thus, the ofp anal. pipeline is an accurate and effective way to construct large representative 'unigene' sets for any plant of interest with no requirement for prior mol. sequence data. The EST sequences are deposited in GenBank/EMBL/DDBJ under accession nos. BQ582276-BQ595857. [This abstract record is one of three records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L21 ANSWER 32 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2002:509980 HCAPLUS
DOCUMENT NUMBER: 137:333832
TITLE: Full-length-enriched cDNA libraries from Echinococcus granulosus contain separate populations of oligo-capped and trans-spliced transcripts and a high level of predicted signal peptide sequences
AUTHOR(S): Fernandez, Cecilia; Gregory, William F.; Loke, P'ng; Maizels, Rick M.
CORPORATE SOURCE: University of Edinburgh, Institute of Cell, Animal and Population Biology, Edinburgh, EH9 3JT, UK
SOURCE: Molecular and Biochemical Parasitology (2002), 122(2), 171-180
CODEN: MBIPDP; ISSN: 0166-6851
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The tissue-dwelling larval stages of the cestode Echinococcus granulosus are intimately associated with the host, implying that a range of mol. mediators may be secreted by the parasite into the host environment. These mediators are being sought through a transcriptome-based anal., using recombinant cDNA libraries. Conventional cDNA libraries of E. granulosus contain high levels of mitochondrial transcripts, as well as host (bovine) genomic DNA. In particular, 60% of a conventional protoscolex stage cDNA library corresponds to the large subunit (LSU) of mitochondrial rRNA. We attribute the presence of LSU rRNA copies to its polyadenylation in E. granulosus. To circumvent this problem, we adapted the 5' Rapid Amplification of cDNA Ends (RNA-ligase mediated RACE) technique that excludes all polynucleotides missing the 7-methyl-guanosine (7MG) cap specific to the 5' end of full-length mRNA. By ligating a specific oligonucleotide (oligo-cap) to 7MG-bearing mRNA, three cDNA libraries were made by **PCR** from oligo-cap and oligo-dT primers. Anal. of these libraries showed that mitochondrial RNA contaminants had been excluded. Moreover, no bovine genomic sequences were detected. In parallel, we constructed three cDNA libraries using the newly described trans-spliced leader (SL) from Echinococcus. Although these represent a smaller subset of parasite genes, mitochondrial and genomic contributions were again excluded. In both cases, a majority of cDNAs (61-92%) were judged to contain the initiation ATG codon, and 11-27% of inserts included potential N-terminal signal sequences. The 5' UTR tracts of most oligo-capped cDNAs were <100 nt, although .apprx.8% were longer than this. Among the trans-spliced cDNAs, 43% potentially utilize the AUG donated by the SL, and in only 6% was the SL separated from an endogenous putative start

site by >60 nt. Sequence anal. of **randomly** selected clones shows virtually no overlap between the oligo-capped and SL libraries, indicating that trans-spliced E. granulosus mRNAs appear to be insensitive to the enzymic treatments used to 'oligo-cap' unspliced mRNAs. The oligo-capped and SL strategies represent efficient and complementary pathways to isolate full-length cDNA clones from this cestode parasite and, possibly, from related parasitic flatworms.

REFERENCE COUNT: 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 33 OF 89 MEDLINE on STN DUPLICATE 8
ACCESSION NUMBER: 2002422471 MEDLINE
DOCUMENT NUMBER: PubMed ID: 12177312
TITLE: Novel ceftazidime-resistance beta-lactamases generated by a codon-based mutagenesis method and selection.
AUTHOR: Gaytan Paul; Osuna Joel; Soberon Xavier
CORPORATE SOURCE: Instituto de Biotecnologia/UNAM, Ap. Postal 510-3, Cuernavaca, Morelos 62250, Mexico.. paul@ibt.unam.mx
SOURCE: Nucleic acids research, (2002 Aug 15) 30 (16) e84. Journal code: 0411011. ISSN: 1362-4962.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200209
ENTRY DATE: Entered STN: 20020815
Last Updated on STN: 20021001
Entered Medline: 20020930

AB Four known and nine new ceftazidime-resistance beta-lactamases were generated by a novel, contaminating codon-based mutagenesis approach. In this method, wild-type codons are spiked with a set of mutant codons during **oligonucleotide** synthesis, generating **random** combinatorial **libraries** of **primers** that contain few codon replacements per **variant**. Mutant codons are assembled by tandem addition of a diluted mixture of five Fmoc-dimer amidites to the growing oligo and a mixture of four DMTr-monomer amidites to generate 20 trinucleotides that encode a set of 18 amino acids. Wild-type codons are assembled with conventional chemistry and the whole process takes place in only one synthesis column, making its automation feasible. The **random** and binomial behavior of this approach was tested in the polylinker region of plasmid pUC19 by the synthesis of three **oligonucleotide libraries** mutagenized at different rates and cloned as mutagenic cassettes. Additionally, the method was biologically assessed by mutating six contiguous codons that encode amino acids 237-243 (ABL numbering) of the TEM(pUC19) beta-lactamase, which is functionally equivalent to the clinically important TEM-1 beta-lactamase. The best ceftazidime-recognizing **variant** was a triple mutant, R164H:E240K: R241A, displaying a 333-fold higher resistance than the wild-type enzyme.

L21 ANSWER 34 OF 89 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 2002:713667 SCISEARCH
THE GENUINE ARTICLE: 585CN
TITLE: Novel ceftazidime-resistance beta-lactamases generated by a codon-based mutagenesis method and selection - art. number e84
AUTHOR: Gaytan P (Reprint); Osuna J; Soberon X
CORPORATE SOURCE: UNAM, Inst Biotechnol, Ap Postal 510-3, Cuernavaca 62250, Morelos, Mexico (Reprint); UNAM, Inst Biotechnol,

Cuernavaca 62250, Morelos, Mexico
COUNTRY OF AUTHOR: Mexico
SOURCE: NUCLEIC ACIDS RESEARCH, (15 AUG 2002) Vol. 30, No. 16, pp. E84-E84.
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND.
ISSN: 0305-1048.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 36

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Four known and nine new ceftazidime-resistance beta-lactamases were generated by a novel, contaminating codon-based mutagenesis approach. In this method, wild-type codons are spiked with a set of mutant codons during **oligonucleotide** synthesis, generating **random** combinatorial **libraries** of **primers** that contain few codon replacements per **variant**. Mutant codons are assembled by tandem addition of a diluted mixture of five Fmoc-dimer amidites to the growing oligo and a mixture of four DMTr-monomer amidites to generate 20 trinucleotides that encode a set of 18 amino acids. Wild-type codons are assembled with conventional chemistry and the whole process takes place in only one synthesis column, making its automation feasible. The **random** and binomial behavior of this approach was tested in the polylinker region of plasmid pUC19 by the synthesis of three **oligonucleotide libraries** mutagenized at different rates and cloned as mutagenic cassettes. Additionally, the method was biologically assessed by mutating six contiguous codons that encode amino acids 237-243 (ABL numbering) of the TEMpUC19 beta-lactamase, which is functionally equivalent to the clinically important TEM-1 beta-lactamase. The best ceftazidime-recognizing **variant** was a triple mutant, R164H:E240K: R241A, displaying a 333-fold higher resistance than the wild-type enzyme.

L21 ANSWER 35 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 9

ACCESSION NUMBER: 2001:676997 HCAPLUS
DOCUMENT NUMBER: 135:237559

TITLE: **Primer** extension **amplification** method for creating libraries of mutagenized nucleic acids

INVENTOR(S): Lietz, Eric
PATENT ASSIGNEE(S): Genopsys, Inc., USA

SOURCE: PCT Int. Appl., 57 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT-NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001066798	A2	20010913	WO 2001-US7016	20010305
WO 2001066798	A3	20021010		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,

Search completed by David Schreiber 308-4292

DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 6319694	B1	20011120	US 2000-518335	20000303
EP 1263987	A2	20021211	EP 2001-916393	20010305
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2002106677	A1	20020808	US 2001-975754	20011010
US 6630329	B2	20031007		

PRIORITY APPLN. INFO.: US 2000-518335 A1 20000303
WO 2001-US7016 W 20010305

AB A method is provided for producing a **library** of mutagenized **polynucleotides** from a target sequence comprising (a) taking a sample comprising: (i) a target sequence including a section to be mutagenized, (ii) a library of first **primers** where the first **primers** include a first **fixed** sequence and a first unknown sequence 3' to the first **fixed** sequence, the first unknown sequence varying within the library of first **primers**, and (iii) a library of second **primers** where the second **primer** include a second **fixed** sequence that differs from the first **fixed** sequence, and a second unknown sequence 3' to the second **fixed** sequence, the second unknown sequence varying within the library of second **primers**; (b) performing one or more cycles of **primer** extension **amplification** on the sample in the presence of at least one polymerase such that a member of the library of the first **primers** is extended relative to the first **primer** that was extended in step (b) to form the **library** of mutagenized **polynucleotides**. The mutagenesis produces a library of mutagenized targeted sequences with **random** truncations, insertions, deletions, or substitutions. The method can be used to generate libraries of nucleic acids encoding proteins which can be screened for clones exhibiting desired biol. characteristics, e.g., stability, solubility, catalytic activity or specificity, binding affinity and specificity, etc., under specified conditions. Thus, the method was applied to mutagenesis of the Bacillus licheniformis penicillinase gene.

L21 ANSWER 36 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2001:137366 HCAPLUS
DOCUMENT NUMBER: 134:188966
TITLE: Method for **random** mutagenesis and amplification of nucleic acid
INVENTOR(S): Lietz, Eric
PATENT ASSIGNEE(S): Genopsys, USA
SOURCE: PCT Int. Appl., 60 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001012802	A1	20010222	WO 2000-US22078	20000811
WO 2001012802	C2	20020711		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

Search completed by David Schreiber 308-4292

Wilder 09/869,891

CROSS REFERENCE: 2003-598271 [56]
DOC. NO. NON-CPI: N2002-091556
DOC. NO. CPI: C2002-037336
TITLE: Selecting a crossover locations in biopolymers, useful for particularly useful designing, engineering and generating new proteins and genes with useful properties, by determining the crossover disruption profiles of biopolymers.
DERWENT CLASS: B04 D16 T01
INVENTOR(S): ARNOLD, F H; MAYO, S L; VOIGT, C A; WANG, Z
PATENT ASSIGNEE(S): (CALY) CALIFORNIA INST OF TECHNOLOGY; (ARNO-I) ARNOLD F H; (MAYO-I) MAYO S L; (VOIG-I) VOIGT C A; (WANG-I) WANG Z
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001090346	A2	20011129	(200216)*	EN	139
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001063411	A	20011203	(200221)		
US 2002045175	A1	20020418	(200228)		
US 2003032059	A1	20030213	(200314)		
EP 1283877	A2	20030219	(200321)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001090346	A2		WO 2001-US16831	20010523
AU 2001063411	A		AU 2001-63411	20010523
US 2002045175	A1	Provisional	US 2000-207048P	20000523
		Provisional	US 2000-235960P	20000927
		Provisional	US 2001-283567P	20010413
			US 2001-863765	20010523
US 2003032059	A1	Provisional	US 2000-207048P	20000523
		Provisional	US 2000-235960P	20000927
		Provisional	US 2001-283567P	20010413
		CIP of	US 2001-863765	20010523
			US 2001-16668	20011026
EP 1283877	A2		EP 2001-937702	20010523
			WO 2001-US16831	20010523

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001063411	A	Based on	WO 2001090346
EP 1283877	A2	Based on	WO 2001090346

PRIORITY APPLN. INFO: US 2001-283567P 20010413; US 2000-207048P 20000523; US 2000-235960P 20000927; US 2001-863765 20010523; US 2001-16668 20011026

Search completed by David Schreiber 308-4292

Wilder 09/869,891

AN 2002-122019 [16] WPIDS
CR 2003-598271 [56]
AB WO 200190346 A UPAB: 20030903
NOVELTY - Selecting a crossover location in a first biopolymer having a first polymer sequence, for recombination with one or more second biopolymers each having its own polymer sequence, comprising determining a crossover disruption related to the number of coupling interactions disrupted in the crossover mutant represented by a data structure, is new.

DETAILED DESCRIPTION - Selecting a crossover location in a first biopolymer having a first polymer sequence, for recombination with one or more second biopolymers each having its own polymer sequence, comprising:

(a) identifying coupling interactions between pairs of residues in the first polymer sequence;

(b) generating several data structures, each data structure representing a crossover mutant comprising a recombination of the first and a second polymer sequence, where each recombination has a different crossover location;

(c) determining, for each data structure, a crossover disruption related to the number of coupling interactions disrupted in the crossover mutant represented by the data structure; and

(d) identifying, among the data structures, a particular data structure having a crossover disruption below a threshold.

The crossover location of the crossover mutant represented by the particular data structure is the identified crossover location.

INDEPENDENT CLAIMS are also included for the following:

(1) a method for directed evolution of a polymer, comprising:

(a) providing parent polymer sequences;

(b) identifying crossover locations in the parent polymer sequences for recombination;

(c) generating one or more mutant polymer sequences using recombinatorial techniques targeted at the identified crossover locations on the parent polymer sequences;

(d) screening the one or more mutant sequences for the one or more properties of interest; and

(e) selecting at least one mutant sequence where one or more properties of interest are identified;

(2) a computer system for analyzing a polymer sequence, comprising a memory and a processor interconnected with the memory and having one or more software components loaded in it, where one or more software components cause the processor to execute steps of the novel method;

(3) a computer program comprising a computer readable medium having one or more software components encoded in computer readable form, where one or more software components may be loaded into a memory of a computer system and cause a processor interconnected with the memory to execute steps of the novel method;

(4) a method for producing hybrid polymers from two or more parent polymers, comprising:

(a) identifying structural domains of at least one parent polymer;

(b) organizing identified domains into schema;

(c) calculating a schema disruption profile;

(d) selecting at least one crossover location based on the schema disruption profile; and

(e) recombining two or more parent polymers at one or more selected crossover locations to produce at least one hybrid polymer;

(5) a method for producing a library of hybrid polymers, comprising:

(a) choosing two or more parent polymers;

(b) identifying structural domains of at least one parent polymer;

(c) organizing identified domains into schema;

(d) calculating a schema disruption profile;

Search completed by David Schreiber 308-4292

(e) selecting crossover locations based on the schema disruption profile;

(f) recombining two or more parent polymers at one or more selected crossover locations to produce a set of hybrid polymers;

(g) repeating at least steps (a) and (f) to produce at least one additional set of hybrid polymers; and

(h) generating a library of hybrid polymers from the sets of hybrid polymers.

(6) a method for modeling the recombination of two or more parent polymers, comprising:

(a) obtaining structural information for at least one parent polymer;

(b) evaluating coupling interactions between polymer residues based on the structural information;

(c) identifying domains based on the determined coupling interactions;

(d) calculating the crossover disruption of the identified domains to produce a disruption profile;

(e) applying a predetermined threshold disruption to each domain of the disruption profile, at least one of accepting domains, which satisfy the threshold, and rejecting domains, which do not satisfy the threshold;

(f) repeating at least the identifying, calculating and applying steps until each identified domain is accepted or rejected;

(g) designating the accepted or rejected domains as disruptive;

(h) selecting crossover regions from domains that are not designated as disruptive; and

(i) recombining parent polymers at selected crossover regions; and

(7) methods of producing recombinant oligonucleotides from two or more parent oligonucleotides by a staggered extension process, an in vitro-in vivo recombination method, a polymerase chain reaction (PCR) amplification method or a family shuffling method.

USE - For the directed evolution of polymers, including directed evolution of nucleic acids and proteins. The methods are particularly useful designing, engineering and generating hybrid biopolymers. The methods are also useful for accelerating the production of new proteins and genes with novel and useful properties.

Dwg.0/27

L21 ANSWER 39 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2002-017486 [02] WPIDS
DOC. NO. NON-CPI: N2002-013974
DOC. NO. CPI: C2002-005011
TITLE: Novel isolated mammalian taste cell-specific G protein-coupled receptor, T2R, involved in bitter taste sensation, useful for identifying taste modulators that are used to decrease or mask bitter taste of foods or drugs.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): ADLER, J E
PATENT ASSIGNEE(S): (SENO-N) SENOMYX INC; (ADLE-I) ADLER J E
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001077676	A1	20011018	(200202)*	EN	103

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ

LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD
SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2001051258 A 20011023 (200213)
US 2002094551 A1 20020718 (200254)
NO 2002004809 A 20021209 (200305)
EP 1292827 A1 20030319 (200322) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
RO SE SI TR
CN 1434921 A 20030806 (200366)
JP 2003530098 W 20031014 (200368) 125

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001077676	A1		WO 2001-US10739	20010404
AU 2001051258	A		AU 2001-51258	20010404
US 2002094551	A1	Provisional	US 2000-195532P	20000407
		Provisional	US 2000-247014P	20001113
			US 2001-825882	20010405
NO 2002004809	A		WO 2001-US10739	20010404
			NO 2002-4809	20021004
EP 1292827	A1		EP 2001-924619	20010404
			WO 2001-US10739	20010404
CN 1434921	A		CN 2001-809145	20010404
JP 2003530098	W		JP 2001-574481	20010404
			WO 2001-US10739	20010404

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001051258	A	Based on	WO 2001077676
EP 1292827	A1	Based on	WO 2001077676
JP 2003530098	W	Based on	WO 2001077676

PRIORITY APPLN. INFO: US 2000-247014P 20001113; US 2000-195532P
20000407; US 2001-825882 20010405
AN 2002-017486 [02] WPIDS
AB WO 200177676 A UPAB: 20020109
NOVELTY - An isolated mammalian taste cell-specific G protein-coupled receptor (GPCR), T2R taste GPCR, (I) involved in bitter taste sensation is new.

DETAILED DESCRIPTION - An isolated mammalian taste cell-specific G protein-coupled receptor (GPCR), T2R taste GPCR, (I) involved in bitter taste sensation is new.

(I) is an isolated polypeptide or fusion protein selected from:

(a) a polypeptide comprising one of the 11 amino acid sequences (S1) defined in the specification;

(b) a polypeptide comprising an amino acid sequence that exhibits 50% identity with S1;

(c) a polypeptide comprising an amino acid sequence that exhibits 75% identity with the fragment of S1 that is at least 40 amino acid in length;

(d) a **chimeric** polypeptide comprising a portion of (a) or (b) that is at least 40 amino acids in length and a portion of at least one other GPCR; or

(e) a **variant** of (a) which differs from the polypeptide by at least one substitution, addition or deletion modification.

INDEPENDENT CLAIMS are also included for the following:

(1) an isolated nucleic acid molecule (II) selected from:

(a) a nucleic acid sequence that comprises one of the 11 nucleotide sequences (S2) defined in the specification or its fragment that comprises at least 75 nucleotides;

(b) an isolated cDNA or an insoluble RNA transcribed from the cDNA that encodes S1, or a fragment of the polynucleotide which encodes at least 25 contiguous amino acids of the polypeptide;

(c) a nucleic acid sequence which is an isolated nucleic acid molecule having at least 20-30%, preferably 90%, sequence identity with S2 or to its fragment which comprises at least 100 contiguous nucleotides;

(d) a nucleic acid sequence which is an isolated nucleic acid molecule that encodes a polypeptide having at least 40%, preferably 99%, sequence identity at the amino acid level with S1 or an isolated nucleic acid molecule encoding at least 40 or 50 contiguous amino acid residues of S1;

(e) a nucleic acid sequence which is an isolated nucleic acid molecule that encodes a taste receptor or its fragment that specifically hybridizes under stringent hybridization conditions to a nucleic acid sequence of S2; and

(f) a nucleic acid sequence which is a **variant** of (a) or (b), containing at least one substitution, deletion or addition mutation in the coding region;

(2) an isolated nucleic acid molecule (III) which encodes for functional taste receptor that comprises a portion of at least 100 nucleotides in length that exhibits at least 40% sequence identity with at least 100 contiguous nucleotides of a portion of S2;

(3) an isolated nucleic acid molecule (IV) comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence of S1;

(4) an expression vector (V) that comprises (II);

(5) a cell (VI) which is transfected or transformed (II);

(6) a solid phase (VII) comprising (II);

(7) a solid phase which is attached to an array of different nucleic acids which includes at least one (II);

(8) a solid phase (VIII) to which is immobilized indirectly or directly at least one (I) or a cell expressing (I) on its surface;

(9) a method of detecting expression of a taste receptor gene, comprising hybridizing at least one sample with (II) and detecting expression of the taste receptor gene by a positive hybridization signal;

(10) a recombinant polynucleotide (IX) comprising (II) which is attached directly or indirectly to a heterologous nucleic acid molecule;

(11) a transfected or transformed cell (X) comprising (IX) introduced into a host cell, or its progeny;

(12) a transgenic non-human organism (XI) comprising (IX) introduced into the cell of a host non-human organism or its progeny;

(13) making (IX) involves (M1) ligating (II) to a heterologous nucleic acid;

(14) making (X) involves introducing (IX) into a host cell, or propagating the host cell in which the recombinant polynucleotide has been introduced;

(15) making (XI) involves introducing (IX) into a cell of a host non-human organism, or propagating the host non-human organism in which the recombinant polynucleotide has been introduced;

(16) an isolated polypeptide molecule (XII) comprising at least 60 contiguous amino acids of S1;

(17) a recombinant polypeptide (XIII) comprising (XII) and a heterologous peptide domain;

(18) an antibody or antibody fragment (XIV) that specifically binds to the polypeptide having an amino acid sequence of S1;

(19) detecting (M2) specific binding of (XIV) to a taste receptor involves contacting the antibody with a sample which may contain the taste receptor and detecting specific binding between them;

(20) an isolated nucleic acid molecule (XV) which exhibits at least 20-30% sequence identity with a fully defined sequence of (S8) or (S9) as given in the specification, or which exhibits at least 30% sequence identity to a fragment comprising at least 100 contiguous nucleotides of the nucleic acid sequence, and which further contains at least one sequence that encodes a polypeptide which is at least 70% identical to a consensus sequence of (S3-S7) identified previously; and

(21) screening a mammalian genome for a coding sequence for GPCR polypeptide active in taste signaling;

(22) a method for detecting specific binding of a putative ligand to a taste receptor;

(23) a method for detecting specific binding of a ligand to a taste receptor which involves contacting the ligand with (XII) and or directly or indirectly detecting specific binding between the ligand and the taste receptor;

(24) a method for screening a library of chemical compounds for compounds that are involved in taste sensation;

(25) a biochemical assay for identifying tastant ligands having binding specificity for a GPCR active in taste signaling;

(26) a method for predicting taste perception in a mammal generated by one or molecules or combinations of molecules using (I);

(27) a cell or non-human animal assay for identifying molecules that interact with a T2R polypeptide;

(28) a method for representing the perception of one or more tastes in one or more mammals;

(29) a method for screening a library which involves hybridizing the library with (XV) and detecting one or more taste receptor clones in the library by a positive hybridization signal; and

(30) a method for detecting expression of a GPCR polypeptide gene in a cell.

USE - (I) is useful for screening one or more compounds for the presence of taste detectable by a mammal. Modulators of (I) (modulators of taste transduction) are useful for pharmacological and genetic modulations of taste signaling pathways. These modulatory compounds are then used in food and pharmaceutical industries to customize taste, e.g., to decrease or mask the bitter taste of foods or drugs. Nucleotide and amino acid sequences of the T2R family members may be used to construct models of taste cell specific polypeptides.

Dwg.0/0

L21 ANSWER 40 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2001-648443 [74] WPIDS

DOC. NO. CPI: C2001-191371

TITLE: Controlling cellular, organismal phenotypes comprises recombining conjoint **polynucleotide** segments to produce recombinant concatamer **library** which is expressed in cells and screened to identify cells with desired phenotype.

DERWENT CLASS: B04 C06 D16

INVENTOR(S): KEENAN, R J; MINSHULL, J; STEMMER, W P C

PATENT ASSIGNEE(S): (KEEN-I) KEENAN R J; (MINS-I) MINSHULL J; (STEM-I) STEMMER W P C; (MAXY-N) MAXYGEN INC

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG

WO 2001073000 A2 20011004 (200174)* EN 93
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW
US 2001049104 A1 20011206 (200203)
AU 2001087273 A 20011008 (200208)
EP 1276861 A2 20030122 (200308) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001073000	A2		WO 2001-US9203	20010323
US 2001049104	A1	Provisional	US 2000-191782P	20000324
		Provisional	US 2001-262617P	20010117
			US 2001-817015	20010323
AU 2001087273	A		AU 2001-87273	20010323
EP 1276861	A2		EP 2001-962421	20010323
			WO 2001-US9203	20010323

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001087273	A	Based on	WO 2001073000
EP 1276861	A2	Based on	WO 2001073000

PRIORITY APPLN. INFO: US 2001-262617P 20010117; US 2000-191782P 20000324; US 2001-817015 20010323

AN 2001-648443 [74] WPIDS

AB WO 200173000 A UPAB: 20011217

NOVELTY - Controlling, (I), a phenotype comprising recombining or mutating a population of conjoint polynucleotide (PN) segments (CPS) comprise, encode or modulate a phenotype, to produce a library, introducing the library into a population of recipient cells or intracellular organelles and identifying a cell, organelle, or organism comprising a cell with a desired phenotype, is new.

DETAILED DESCRIPTION - Controlling (I) a phenotype comprises recombining or mutating a population of conjoint polynucleotide (PN) segments (CPS) where one or more CPS comprise, encode or modulate a phenotype, to produce a library of recombinant concatamers, introducing the library into a population of recipient cells or intracellular organelles and identifying a cell, organelle, or organism comprising a cell with a desired phenotype.

INDEPENDENT CLAIMS are also included for the following:

(1) modulating (II) activity of one or more targets, by providing a library of PN segments encoding several peptides, which are pre-selected for one or more desired properties which are same or different between peptides, joining the pre-selected PN segments to generate a population of CPS which are operably linked to at least one transcription regulatory sequence, expressing one or more of CPS in vitro or in vivo which produces one or more multipeptides comprising several peptide segments which are optionally joined by a linker sequence and identifying one or more CPS

encoding a multipeptide comprising a peptide capable of modulating activity of one or more targets;

(2) producing (III) a library of preselected peptides by providing a library of nucleic acids encoding fusion polypeptides which are capable of displaying one or more variable peptide moieties in vitro or in vivo, expressing the fusion polypeptides such that the one or more variable peptide moieties are displayed in vitro or in vivo and identifying several variable peptide moieties with a desired property which produces a library of pre-selected peptides;

(3) a library of pre-selected peptide produced by the above method;

(4) a library (IV) of nucleic acids comprising several CPS which alter expression of one or more components of an endogenous phenotype, operably linked to a transcription regulatory sequence;

(5) a library comprising population of CPS;

(6) a recombinant episomal vector contained in CPS; and

(7) a cell or an organism comprising a cell produced by (I).

USE - (I) is useful for controlling a phenotype including oil content or composition, fat content or composition, sugar content or composition, starch content or composition, protein content or composition, phytochemical content or composition, nutraceutical content or composition, yield, time to maturity, growth rate, height at maturity, carbon-fixation rate, tolerance to salt, heat, cold, drought, water, heavy metal, radiation, resistance to a chemical composition, disease resistance, insect, parasite resistance, color, fluorescence, height, weight, density, toxicity, flavor, sweetness, bitterness, nutritional activity or therapeutic activity. The phenotype is regulated by at least one epigenetic mechanism such as chromatin silencing, methylation, maternal effects, regulation by cytoplasmic factors, antisense suppression, sense suppression, cosuppression, promoter alteration, DNA recombination, homology-dependent mechanisms, aminoacylation and post-transcriptional gene silencing comprising silencing by a dominant negative inhibitor, a transdominant inhibitor or a peptide inhibitor. (II) is useful for modulating activity of one or more targets comprising a class of enzymes such as proteases, lipases, esterases, hydrolases or amylases, intracellular, extracellular and cell-surface molecules. (III) is useful for producing a library of pre-selected peptides comprising in excess of 100-1000000 different members (all claimed). The multigenic phenotypes modulated include cell cycle state, cell cycle progression, cell morphology, DNA replication activity, transcriptional activity, nucleic acid recombination activity, meiosis, timing and quantity of secondary metabolite production.

ADVANTAGE - The method provides simple and rapid processes for screening and optimizing peptides that modulate the activity of cellular targets such as enzymes.

DESCRIPTION OF DRAWING(S) - The figure shows the schematic illustration showing the correspondence of multiple genetic elements that make up an episomal vector comprising conjoint polynucleotide segments with multiple genes of a genetic or metabolic pathway.

Dwg.1/6

L21 ANSWER 41 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2001-570867 [64] WPIDS
CROSS REFERENCE: 2002-083330 [11]
DOC. NO. CPI: C2001-169764
TITLE: Nucleic acids encoding human olfactory G protein-coupled receptors, useful for screening for compounds involved in olfactory sensation, where the compounds can be used in the food, pharmaceutical and cosmetic industries to customize odors.

Search completed by David Schreiber 308-4292

Wilder 09/869,891

DERWENT CLASS: B04 D13 D16 D21
INVENTOR(S): ZOZULYA, S
PATENT ASSIGNEE(S): (SENO-N) SENOMYX INC; (ZOZU-I) ZOZULYA S
COUNTRY COUNT: 96
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001068805	A2	20010920	(200164)*	EN	320
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TR TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW					
AU 2001047366	A	20010924	(200208)		
EP 1299528	A1	20030409	(200325)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI TR					
US 2003088059	A1	20030508	(200337)		
JP 2004504010	W	20040212	(200413)		901

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2001068805	A2		WO 2001-US7771	20010313
AU 2001047366	A		AU 2001-47366	20010313
EP 1299528	A1		EP 2001-920295	20010313
			WO 2001-US7771	20010313
US 2003088059	A1	Provisional	US 2000-188914P	20000313
		Provisional	US 2000-192033P	20000324
		Provisional	US 2000-198474P	20000412
		Provisional	US 2000-199335P	20000424
		Provisional	US 2000-207702P	20000526
		Provisional	US 2000-213849P	20000623
		Provisional	US 2000-226534P	20000816
		Provisional	US 2000-230732P	20000907
		Provisional	US 2001-266862P	20010207
			US 2001-804291	20010313
JP 2004504010	W		JP 2001-567289	20010313
			WO 2001-US7771	20010313

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001047366	A	Based on	WO 2001068805
EP 1299528	A1	Based on	WO 2001068805
JP 2004504010	W	Based on	WO 2001068805

PRIORITY APPLN. INFO: US 2001-266862P 20010207; US 2000-188914P 20000313; US 2000-192033P 20000324; US 2000-198474P 20000412; US 2000-199335P 20000424; US 2000-207702P 20000526; US 2000-213849P 20000623; US 2000-226534P 20000816; US 2000-230732P 20000907; US 2001-804291 20010313
AN 2001-570867 [64] WPIDS

Search completed by David Schreiber 308-4292

CR 2002-083330 [11]
AB WO 200168805 A UPAB: 20040223
NOVELTY - Nucleic acids encoding human olfactory G protein-coupled receptors, are new.

DETAILED DESCRIPTION - Nucleic acids encoding human olfactory G protein-coupled receptors, are new.

A nucleic acid (N1) encoding the human olfactory G protein-coupled receptor is selected from:

(a) an isolated nucleotide sequence selected from one of the 256 nucleotide sequences (N2) defined in the specification or its fragment which comprises at least 75 nucleotides;

(b) an isolated cDNA or an insoluble RNA transcribed from it that encodes a polypeptide having one of the 256 amino acid sequences (P1) defined in the specification, or its fragment which encodes at least 25 contiguous amino acids of the polypeptide;

(c) a nucleic acid sequence that comprises at least 30-90%, preferably 90%, sequence identity with an isolated nucleic acid sequence selected from N2, or its fragment which comprises at least 100 contiguous nucleotides;

(d) a nucleic acid sequence that encodes a polypeptide having at least 40-99% sequence identity at the amino acid level with a polypeptide having an amino acid sequence selected from P1 or its fragment comprising at least 40 contiguous amino acids that optionally is directly or indirectly attached to a sequence that facilitates the expression and/or translocation of the polypeptide on the surface of the cell, or a nucleotide sequence encoding at least 40 or 50 contiguous amino acid residues of the polypeptide;

(e) an isolated nucleic acid sequence which encodes an olfactory receptor or its fragment that specifically hybridizes and exhibits at least 30% sequence identity under stringent conditions to a nucleic acid sequence selected from N2;

(f) an isolated nucleic acid sequence that specifically hybridizes to the nucleic acid of (a) or its portion under stringent hybridization conditions that is at least 20-30 nucleotide in length; or

(g) a naturally occurring allelic or synthetic **variant** of a nucleic acid sequence of (a) or (b), containing at least one substitution, deletion or addition mutation in the coding region.

INDEPENDENT CLAIMS are included for the following:

(1) an isolated nucleic acid which exhibits at least 50%, 60%, 70%, 80%, 85%, 90%, 95% or 96-99% sequence identity with a nucleic acid selected from N2 or a nucleic acid sequence which exhibits at least 50%, 60%, 70%, 80%, 85%, 90%, 95% or 96-99% sequence identity to a fragment comprising at least 100 contiguous nucleotides of the nucleic acid sequence;

(2) a nucleic acid sequence (N3) which encodes for a functional olfactory receptor polypeptide;

(3) an isolated nucleic acid (N4) comprising a nucleotide sequence that encodes a fragment of at least 60 contiguous amino acids of a polypeptide having an amino acid sequence selected from P1;

(4) an expression vector that comprises N1 and optionally an operably linked heterologous nucleic acid that drives its expression;

(5) a cell (C1) which is transfected or transformed with N1;

(6) a solid phase comprising N1, where the solid phase is attached to an array comprising at least one additional nucleic acid sequence;

(7) an isolated polypeptide (P2) that is selected from:

(a) a polypeptide comprising an amino acid sequence selected from P1;

(b) a polypeptide comprising an amino acid sequence that exhibits at least 40-99% sequence identity with an amino acid selected from P1;

(c) a polypeptide comprising an amino acid sequence that exhibits at

least 60% sequence identity with a fragment of the polypeptide of (a), where the fragment is at least 40 amino acids in length;

(d) a **chimeric** polypeptide that comprises a portion of a polypeptide of (a) or (b) that is at least 40 amino acids in length and a portion of at least one other G protein-coupled receptor; or

(e) a **variant** of the polypeptide of (a) which differs with the polypeptide by at least one substitution, addition or deletion modification;

(8) a solid phase comprising at least one directly or indirectly immobilized P2, or a cell which expresses the polypeptide on its surface;

(9) a method of detecting expression of an olfactory receptor gene;

(10) a method of screening a library comprising hybridizing the library with N1 and detecting one or more olfactory receptor clones in the library by a positive hybridization signal;

(11) a recombinant polynucleotide (N4) comprising N1 attached directly or indirectly to a heterologous nucleic acid;

(12) a transfected or transformed cell comprising N4 introduced into a host cell, or its progeny;

(13) a transgenic non-human organism comprising N4 introduced into a cell of a host non-human organism, or its progeny;

(14) a method (M1) of making a recombinant polynucleotide comprising ligating N1 to a heterologous nucleic acid;

(15) a method of making a transfected cell;

(16) a method of detecting specific binding of a putative ligand to an olfactory receptor;

(17) a method of making transgenic non-human organism;

(18) an isolated protein (P3) comprising a fragment of at least 60 contiguous amino acids having an amino acid sequence selected from P1;

(19) a recombinant polypeptide (P4) comprising P3 and a heterologous peptide domain;

(20) a method of detecting specific binding of a ligand to an olfactory receptor;

(21) an antibody (AB1) or its fragment that specifically binds a polypeptide having an amino acid sequence selected from P1;

(22) a method (M2) of detecting specific binding of AB1 to an olfactory receptor;

(23) a method (M3) of screening a library of chemical compounds for compounds that are involved in olfactory sensation;

(24) a cell-based assay (M4) for identifying molecules that interact with an olfactory receptor;

(25) a method (M5) for representing the olfactory perception of one or more odors in one or more mammals; and

(26) a method (M6) for predicting the odor perception in a mammal generated by one or more molecules or combinations of molecules.

ACTIVITY - None given.

No biological data given.

MECHANISM OF ACTION - Olfactory G protein-coupled receptor modulators.

No biological data given.

USE - The human olfactory G protein-coupled receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation.

The modulators are useful for pharmacological and genetic modulation of olfactory signaling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customize odors and fragrances.

Dwg.0/5

L21 ANSWER 42 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2001-300506 [31] WPIDS

Search completed by David Schreiber 308-4292

(4) producing a **polynucleotide library** (M3) comprising:

(a) constructing a first and second parent polynucleotide construct, each comprising a region encoding for a polypeptide, an upstream **primer**, and a downstream **primer**, where one **primer** of the first polynucleotide construct comprises a restriction site for a first restriction enzyme, and the other **primer** comprises a restriction site for a second restriction enzyme, and one **primer** of the second polynucleotide construct comprises a restriction site for the second restriction enzyme;

(b) cutting the polynucleotide constructs with a mixture of restriction enzymes, the first polynucleotide construct being cut with the first and second restriction enzymes, and the second polynucleotide construct being cute with the second and third restriction enzymes;

(c) cutting a vector with the first and third restriction enzymes;

(d) ligating the first polynucleotide construct, the second polynucleotide construct, and the vector, to form a vector construct comprising a polynucleotide dimer connected by a linker sequence;

(e) **amplifying** the vector construct by **polymerase chain reaction** (**PCR**);

(f) excising a polynucleotide dimer from the **amplified** vector by cutting with the first and third restriction enzymes;

(g) digesting the polynucleotide dimer;

(h) selecting digested polynucleotide dimers of a predetermined size; and

(i) circularizing the selected digested polynucleotide dimers to from a circular construct;

(5) producing a **polynucleotide library** (M4) comprising:

(a) preparing a first polynucleotide construct comprising at least two parent polynucleotides connected by a linker sequence comprising at least one restriction site;

(b) digesting the first construct;

(c) creating a first **polynucleotide library** by selecting fragments of the first digested polynucleotide construct which approximate a predetermined size;

(d) preparing a second polynucleotide construct comprising at least the two parent polynucleotides connected by a linker sequence comprising at least one restriction site, where the polynucleotides are placed in opposite order than in the first polynucleotide construct;

(e) digesting the second construct;

(f) creating a second **polynucleotide library** by selecting fragments of the second digested polynucleotide construct, which approximate a predetermined sized; and

(g) creating a third **polynucleotide library** by shuffling the first and second **polynucleotide library** together;

(6) producing a protein library (M5) comprising:

(a) preparing a polynucleotide construct comprising at least two parent polynucleotides connected by a linker sequence, where the linker sequence comprises a restriction site for at least one restriction enzyme;

(b) digesting the construct;

(c) selecting fragments of the digested polynucleotide construct which approximate a predetermined size;

(d) linearizing the circular fragments by cutting the restriction enzyme;

(e) inserting the linearized fragments into an expression vector; and

(f) expressing the vector in an expression system;

(7) a protein produced by (M5);

(8) a protein expressed from a vector comprising a linearized circular polynucleotide construct comprising polynucleotide sequences from at least two parent polynucleotides, where the N-terminal of a first parent polynucleotide is linked to the C-terminal of a second parent polynucleotide via a linker sequence;

(9) a circular polynucleotide construct comprising polynucleotide sequences from at least two parent polynucleotides, where the N-terminal of a first parent polynucleotide is linked to the C-terminal of a second parent polynucleotide via a linker sequence;

(10) an expression vector produced by a method comprising the steps of linearizing the circular polynucleotide construct in (9) by treatment with the restriction enzyme, and inserting the linearized polynucleotide construct into an expression vector;

(11) a protein expressed from the vector in (9);

(12) a circular polynucleotide construct comprising polynucleotide sequences from at least two parent polynucleotides where:

(a) at least two polynucleotide sequences are connected by a linker sequence;

(b) at least two polynucleotide sequences are truncated; and

(c) the size of the polynucleotide sequences together approximate a predetermined size;

(13) an expression vector produced by a method as in (10) by linearizing the construct of (12);

(14) vector construct comprising a polynucleotide encoding a chimeric protein and a stop codon in each of three reading frames positioned proximal to the 3' end of the polynucleotide, where the polynucleotide comprises one segment encoding the C-terminal end of a first parent protein and one segment encoding the N-terminal end of a second parent protein;

(15) a library of hybrid proteins comprising polypeptide sequences from at least two parent proteins, where the hybrid proteins comprise an N-terminal sequence corresponding to the N-terminal sequence of a first parent protein, and a C-terminal sequence corresponding to the C-terminal sequence of a second parent protein;

(16) a protein encoded by a nucleotide sequence selected from the group of 5 sequences described in the specification;

(17) producing a gene library comprising steps (a)-(c) of (M1);

(18) producing a gene library comprising the steps as in (M3);

USE - The present invention provides an improved method for creating gene and protein libraries. The invention can be used to make random libraries of circularly permuted variants of genes encoding a single protein, or hybrid proteins containing fragments from two or more parent proteins. The invention can also be used to create a library for protein fragment complementation, in which fragments originate either from one protein or form different proteins, typically from two proteins.

ADVANTAGE - The invention provides techniques for preserving or recreating the original N- and C-terminal sequences of the parent protein(s).

Dwg.0/15

L21 ANSWER 43 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2001-282160 [29] WPIDS
CROSS REFERENCE: 2001-290916 [30]
DOC. NO. CPI: C2001-086067
TITLE: Forming double-stranded **chimeric** polynucleotide, comprises hybridizing double-stranded template containing two single-stranded regions with population of oligonucleotides and treating hybridized oligonucleotides.

Search completed by David Schreiber 308-4292

Wilder 09/869,891

DERWENT CLASS: B04 D16
INVENTOR(S): ARENSDORF, J J; COCO, W M
PATENT ASSIGNEE(S): (ENCH-N) ENCHIRA BIOTECHNOLOGY CORP
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001029212	A1	20010426	(200129)*	EN	52

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2001010980 A 20010430 (200148)
AU 2001021173 A 20010430 (200148)

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001029212	A1	WO 2000-US41319	20001019
AU 2001010980	A	AU 2001-10980	20001019
AU 2001021173	A	AU 2001-21173	20001019

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001010980	A	Based on	WO 2001029211
AU 2001021173	A	Based on	WO 2001029212

PRIORITY APPLN. INFO: US 2000-219062 20000718; US 1999-160420P 19991019; US 2000-514660 20000229; US 2000-218883 20000718; US 2000-219087 20000718; US 2000-219090 20000718; US 2000-618696 20000718; US 2000-618935 20000718

AN 2001-282160 [29] WPIDS
CR 2001-290916 [30]
AB WO 200129212 A UPAB: 20011129
NOVELTY - Forming (M1) a double-stranded (ds) **chimeric** polynucleotide comprising contacting a double-stranded polynucleotide template containing at least two single-stranded (ss) regions with a population of oligonucleotides such that at least one oligonucleotide hybridizes to each ss region, and treating the template and hybridized oligonucleotide to form ds **chimeric** polynucleotide, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a **chimeric** polynucleotide (I) prepared by M1; and

(2) preparing (M2) a ds polynucleotide template suitable for use in M1, involves treating a ds polynucleotide such that at least two ss nicks are introduced, and treating the nicked polynucleotide such that a ss region of the polynucleotide is formed at each nick, resulting in a ds polynucleotide suitable for use in M1.

USE - M1 is useful for forming a **chimeric** double-stranded polynucleotide (claimed). M1 is useful for generating **libraries** of **chimeric** double-stranded **polynucleotides** containing genotypic **variants** that have desired properties (phenotype) that

are improved with respect to parental phenotypes. M1 is useful for evolving industrially or medically useful molecules, biochemical pathways, or regulatory sequence.

DESCRIPTION OF DRAWING(S) - The figure shows the schematic diagram of the formation of double-stranded **chimeric** polynucleotide.

Dwg.1/1

L21 ANSWER 44 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2001-266320 [27] WPIDS

DOC. NO. CPI: C2001-080711

TITLE: Production of recombinant adenovirus, useful e.g. in gene therapy and genomics, by homologous recombination between parent and shuttle plasmids.

DERWENT CLASS: B04 D16

INVENTOR(S): ROBERT, J

PATENT ASSIGNEE(S): (AVET) AVENTIS PHARMA SA

COUNTRY COUNT: 95

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001025463	A1	20010412	(200127)*	FR	70
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
FR 2799472	A1	20010413	(200129)		
AU 2000077947	A	20010510	(200143)		
BR 2000014489	A	20020604	(200246)		
NO 2002001634	A	20020604	(200250)		
EP 1224310	A1	20020724	(200256)	FR	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
CZ 2002001215	A3	20020814	(200263)		
KR 2002057969	A	20020712	(200305)		
CN 1384885	A	20021211	(200324)		
HU 2002003801	A2	20030328	(200333)		
JP 2003512823	W	20030408	(200333)		73
ZA 2002002481	A	20030923	(200368)		107
MX 2002003247	A1	20021001	(200370)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001025463	A1	WO 2000-FR2774	20001005
FR 2799472	A1	FR 1999-12521	19991007
AU 2000077947	A	AU 2000-77947	20001005
BR 2000014489	A	BR 2000-14489	20001005
		WO 2000-FR2774	20001005
NO 2002001634	A	WO 2000-FR2774	20001005
		NO 2002-1634	20020405
EP 1224310	A1	EP 2000-967960	20001005
		WO 2000-FR2774	20001005
CZ 2002001215	A3	WO 2000-FR2774	20001005
		CZ 2002-1215	20001005
KR 2002057969	A	KR 2002-704452	20020406

CN 1384885	A	CN 2000-814903	20001005
HU 2002003801	A2	WO 2000-FR2774	20001005
		HU 2002-3801	20001005
JP 2003512823	W	WO 2000-FR2774	20001005
		JP 2001-528614	20001005
ZA 2002002481	A	ZA 2002-2481	20020327
MX 2002003247	A1	WO 2000-FR2774	20001005
		MX 2002-3247	20020327

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000077947	A	Based on	WO 2001025463
BR 2000014489	A	Based on	WO 2001025463
EP 1224310	A1	Based on	WO 2001025463
CZ 2002001215	A3	Based on	WO 2001025463
HU 2002003801	A2	Based on	WO 2001025463
JP 2003512823	W	Based on	WO 2001025463
MX 2002003247	A1	Based on	WO 2001025463

PRIORITY APPLN. INFO: US 1999-168356P 19991201; FR 1999-12521 19991007

AN 2001-266320 [27] WPIDS

AB WO 200125463 A UPAB: 20010518

NOVELTY - Production of adenovirus (AdV) by homologous recombination between shuttle plasmid (P1) and parent plasmid (P2) to produce a final plasmid (P3) containing a complete, recombinant AdV genome. This genome is excised as a linear sequence and inserted into a prokaryotic packaging cells to produce AdV containing a complete genome.

DETAILED DESCRIPTION - Production of adenovirus (AdV) by homologous recombination between shuttle plasmid (P1) and parent plasmid (P2) to produce a final plasmid (P3) containing a complete, recombinant AdV genome. This genome is excised as a linear sequence and inserted into a prokaryotic packaging cells to produce AdV containing a complete genome. P1, preferably prokaryotic, contains a truncated AdV genome and at least one heterologous nucleic acid (I) and P2 contains a truncated AdV genome, complementary to that in P1.

INDEPENDENT CLAIMS are also included for the following:

(a) P1 that contains an AdV ITR (inverted terminal repeat), (I) (or a site for its introduction) and an AdV homology sequence, with ITR **flanked** by a restriction site not present in the AdV genome;

(b) nucleic acid library cloned in P1;

(c) P2;

(d) cells containing one or more of P1 and P2;

(e) a method for preparing AdV libraries;

(f) AdV libraries produced by method (e) comprising AdV containing nucleic acid inserts from:

(i) library of cDNA, genomic DNA or synthetic DNA;

(ii) a **library** of (semi-)**random oligonucleotides**; or

(iii) a library of sequences able to bind to DNA; and

(g) kits containing P1 and P2.

ACTIVITY - None given.

MECHANISM OF ACTION - Gene therapy.

USE - The method is used to produce expression libraries of AdV, useful:

(i) for studying the function of clones in the library; and

(ii) for screening for genes (potential therapeutic targets).

Search completed by David Schreiber 308-4292

AdV may also be used to determine the biological functions of nucleic acid or proteins, as vectors for gene therapy (expressing a wide variety of therapeutic proteins or vaccinating antigens) and for recombinant production of proteins (e.g. interferons, antibodies and insulin).

ADVANTAGE - AdV can now be produced simply, rapidly, efficiently and in large quantities, in an automated process. Particularly the method does not require a multiple-selection screening step (rather a single-step selection) and neither of the starting plasmids are, alone, able to generate a functional virus, only the homologous recombination product.

Dwg.0/11

L21 ANSWER 45 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2001-212739 [22] WPIDS
DOC. NO. CPI: C2001-063590
TITLE: New synthetic oligobodies that behave like natural antibodies and recognize both native and denatured proteins, useful in protein purification, affinity chromatography, library screening or for treating tumors.
DERWENT CLASS: B04 D16
INVENTOR(S): SANTA COLOMA, T A
PATENT ASSIGNEE(S): (COLO-I) SANTA COLOMA T A
COUNTRY COUNT: 28
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
EP 1078992	A2	20010228	(200122)*	EN	31
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
JP 2001120282	A	20010508	(200131)		19
BR 2000003768	A	20010703	(200141)		
MX 2000008256	A1	20020501	(200368)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
EP 1078992	A2	EP 2000-307252	20000823
JP 2001120282	A	JP 2000-252476	20000823
BR 2000003768	A	BR 2000-3768	20000823
MX 2000008256	A1	MX 2000-8256	20000823

PRIORITY APPLN. INFO: AR 1999-104272 19990826
AN 2001-212739 [22] WPIDS
AB EP 1078992 A UPAB: 20010421

NOVELTY - New synthetic oligonucleotide-based antibody-like reagents (oligobodies) comprising natural or derivatized oligonucleotides selected based on high specificity rather than high affinity, which possess unique ability to behave like natural polyclonal or monoclonal antibodies in their multiple applications, recognizing both native and denatured proteins in a very specific way, are new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) obtaining (M1) an oligobody;

(2) an oligobody (I) comprising oligonucleotides, which bind specifically to a target protein, obtained by M1;

(3) an article of manufacture comprising a solid matrix having attached to it (I);

(4) oligobodies comprising products made of nucleic acids of double or single strands, or ribonucleic acids or deoxyribonucleic acids having natural or modified chemical groups;

(5) oligobodies obtained using as temporary target:

(a) a fragment of the final target, which could be any polymer (protein, carbohydrate, oligonucleotides, etc.) or molecule of importance for biotechnology, research or clinics; or

(b) a modified synthetic peptide (such as phosphorylated, isoprenylated, glycosylated);

(6) selecting (M2) a mixture of oligonucleotides, each capable of specifically binding a target molecule;

(7) selecting (M3) an oligonucleotide capable of acting as a monoclonal antibody by specifically binding to a target comprising selecting a mixture of oligonucleotides, and selecting an oligonucleotide from the mixture to its capacity to bind to a target molecule;

(8) a mixture of oligonucleotides, which is capable of specifically binding a target, obtained with M2;

(9) an oligonucleotide obtained for M3 that is capable of acting as a monoclonal antibody be specifically binding a target and having a sequence length of 30-200 nucleotides; and

(10) a kit for use in a diagnostic method containing an oligobody or an oligonucleotide comprising an oligobody or oligonucleotide, by constructing the oligobody or oligonucleotide in an oligonucleotide synthesizer.

ACTIVITY - Cytostatic.

MECHANISM OF ACTION - None given.

USE - The oligobodies are useful in protein purification, affinity chromatography, library screening, cell sorting, confocal microscopy, in medicine, as a pharmaceutical carrier, or in the manufacture of an agent effective as a physiological inhibitor or activator (claimed). The oligobodies can replace natural monoclonal or polyclonal antibodies in diagnostic tests, immunohistochemistry or immunoprecipitations. The oligobodies may be used in the treatment of tumors and other diseases where monoclonal antibodies have failed.

ADVANTAGE - Compared to monoclonal antibodies, oligobodies have the advantage of rapid design and production, low cost, high affinity, independence of the immune system (these do not require the target to be antigenic), and better diffusibility (since these are at least 5-fold smaller than natural antibodies). These may be produced easily against different region of a target protein, independently of their antigenicity. Chips similar to those used for DNA can be easily produced for use in diagnosis, gene expression studies, etc.

Dwg.0/11

L21 ANSWER 46 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	2001:456914 HCAPLUS
DOCUMENT NUMBER:	135:283675
TITLE:	Hybridization to high-density filter arrays of a Brugia malayi BAC **library** with biotinylated **oligonucleotides** and **PCR** products
AUTHOR(S):	Foster, J. M.; Kamal, I. H.; Daub, J.; Swan, M. C.; Ingram, J. R.; Ganatra, M.; Ware, J.; Guiliano, D.; Aboobaker, A.; Moran, L.; Blaxter, M.; Slatko, B. E.
CORPORATE SOURCE:	New England Biolabs, Beverly, MA, USA
SOURCE:	BioTechniques (2001), 30(6), 1216-1224 CODEN: BTNQDO; ISSN: 0736-6205
PUBLISHER:	Eaton Publishing Co.
DOCUMENT TYPE:	Journal
LANGUAGE:	English

Search completed by David Schreiber 308-4292

AB The use of nonradioactive hybridization and chemiluminescent detection procedures for genome mapping was extended to high d. filter arrays. To increase genome mapping throughput, nonradioactive hybridization methods with biotinylated oligonucleotides or **polymerase chain reaction** (**PCR**) products, generated using biotinylated primers for use as probes, were utilized. These methods maintain the hybridization fidelity and high signal to noise ratio observed with probes prepared by **random** printing. The procedure is robust and no major equipment such as CCD cameras or scanners is required.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 47 OF 89 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN DUPLICATE 10

ACCESSION NUMBER: 2001132989 EMBASE
TITLE: DNA shuffling method for generating highly recombined genes and evolved enzymes.
AUTHOR: Coco W.M.; Levinson W.E.; Crist M.J.; Hektor H.J.; Darzins A.; Pienkos P.T.; Squires C.H.; Monticello D.J.
CORPORATE SOURCE: W.M. Coco, Enchira Biotechnology Corporation, 4200 Research Forest Drive, The Woodlands, TX 77381, United States. wcoco@enchira.com
SOURCE: Nature Biotechnology, (2001) 19/4 (354-359).
Refs: 37
ISSN: 1087-0156 CODEN: NABIF
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 004 Microbiology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB We introduce a method of in vitro recombination or "DNA shuffling" to generate libraries of evolved enzymes. The approach relies on the ordering, trimming, and joining of **randomly** cleaved parental DNA fragments annealed to a transient **polynucleotide** scaffold. We generated chimeric **libraries** averaging 14.0 crossovers per gene, a several-fold higher level of recombination than observed for other methods. We also observed an unprecedented four crossovers per gene in regions of 10 or fewer bases of sequence identity. These properties allow generation of chimeras unavailable by other methods. We detected no unshuffled parental clones or duplicated "sibling" chimeras, and relatively few inactive clones. We demonstrated the method by molecular breeding of a monooxygenase for increased rate and extent of biodesulfurization on complex substrates, as well as for 20-fold faster conversion of a nonnatural substrate. This method represents a conceptually distinct and improved alternative to sexual **PCR** for gene family shuffling.

L21 ANSWER 48 OF 89 MEDLINE on STN DUPLICATE 11

ACCESSION NUMBER: 2001159568 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11233988
TITLE: Mapping of RNA accessible sites by extension of **random oligonucleotide libraries** with reverse transcriptase.
AUTHOR: Allawi H T; Dong F; Ip H S; Neri B P; Lyamichev V I
CORPORATE SOURCE: Third Wave Technologies, Inc., Madison, Wisconsin 53719, USA.
SOURCE: RNA (New York, N.Y.), (2001 Feb) 7 (2) 314-27.
Journal code: 9509184. ISSN: 1355-8382.
PUB. COUNTRY: United States

Search completed by David Schreiber 308-4292

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010322

AB A rapid and simple method for determining accessible sites in RNA that is independent of the length of target RNA and does not require RNA labeling is described. In this method, target RNA is allowed to hybridize with sequence-**randomized libraries** of DNA **oligonucleotides** linked to a common tag sequence at their 5'-end. Annealed oligonucleotides are extended with reverse transcriptase and the extended products are then amplified by using **PCR** with a primer corresponding to the tag sequence and a second primer specific to the target RNA sequence. We used the combination of both the lengths of the RT-**PCR** products and the location of the binding site of the RNA-specific primer to determine which regions of the RNA molecules were RNA extendible sites, that is, sites available for oligonucleotide binding and extension. We then employed this reverse transcription with the **random oligonucleotide libraries** (RT-ROL) method to determine the accessible sites on four mRNA targets, human activated ras (ha-ras), human intercellular adhesion molecule-1 (ICAM-1), rabbit beta-globin, and human interferon-gamma (IFN-gamma). Our results were concordant with those of other researchers who had used RNase H cleavage or hybridization with arrays of oligonucleotides to identify accessible sites on some of these targets. Further, we found good correlation between sites when we compared the location of extendible sites identified by RT-ROL with hybridization sites of effective antisense oligonucleotides on ICAM-1 mRNA in antisense inhibition studies. Finally, we discuss the relationship between RNA extendible sites and RNA accessibility.

L21 ANSWER 49 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 12
ACCESSION NUMBER: 2000:513826 HCAPLUS
DOCUMENT NUMBER: 133:130745
TITLE: Process for the generation of **oligonucleotide libraries** (OLS) representative of genomes or expressed mRNAs (cDNAs) and uses thereof
INVENTOR(S): **Paquin, Bruno**; Brukner, Ivan; Tremblay, Guy
PATENT ASSIGNEE(S): Universite de Montreal, Can.
SOURCE: PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000043538	A1	20000727	WO 2000-CA47	20000119

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,

Search completed by David Schreiber 308-4292

CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
CA 2360567 AA 20000727 CA 2000-2360567 20000119
EP 1144683 A1 20011017 EP 2000-900999 20000119
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
PRIORITY APPLN. INFO.: CA 1999-2259745 A 19990119
WO 2000-CA47 W 20000119

AB A process for the generation of **oligonucleotide libraries** representative of a given template is described. The process starts from a pool of oligonucleotides that contain a core sequence that is **random** and **flanked** by uniform sequences designed not to hybridize with the nucleic acids of interest. Hybridization is used to select only those sequences that hybridize to the template nucleic acid. This selection yields a highly specific library that represents an image of the chosen template in oligonucleotides. The novel quality of this approach is the generation of amplifiable oligonucleotide probes that are of uniform length, free of repetitive sequence motifs and easily subjected to differential selection. This technique is used to produce different **oligonucleotide libraries** (OLs) and shows that these OLs do not cross-hybridize. Differential selection of these OLs produces oligonucleotides that can be used in the identification, characterization and isolation of nucleic acids.

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 50 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:646133 HCAPLUS
DOCUMENT NUMBER: 133:233579
TITLE: In vitro evolution of protein properties using methods of saturating mutagenesis and high throughput screening and selection for specific properties
INVENTOR(S): Short, Jay M.; Frey, Gerhard Johann
PATENT ASSIGNEE(S): Diversa Corporation, USA
SOURCE: PCT Int. Appl., 259 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 40
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000053744	A2	20000914	WO 2000-US6497	20000309
WO 2000053744	A3	20010118		
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6238884	B1	20010529	US 1999-267118	19990309
US 6352842	B1	20020305	US 1999-276860	19990326
US 6537776	B1	20030325	US 1999-332835	19990614
AU 2000038793	A5	20000928	AU 2000-38793	20000309
EP 1161529	A2	20011212	EP 2000-917887	20000309

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

JP 2002537836	T2	20021112	JP 2000-603365		20000309
AU 756201	B2	20030109	AU 2000-48933		20000731
AU 2000048933	A5	20001005			
US 2002086279	A1	20020704	US 2001-875412		20010606
US 6677115	B2	20040113			
US 2003219752	A1	20031127	US 2002-151469		20020517

PRIORITY APPLN. INFO.:

US 1999-267118	A	19990309
US 1999-276860	A	19990326
US 1999-332835	A	19990614
US 1995-8311P	P	19951207
US 1995-8316P	P	19951207
US 1996-651568	A2	19960522
US 1996-677112	A2	19960709
US 1996-760489	A1	19961205
AU 1997-11489	A3	19961206
US 1997-962504	B2	19971031
US 1997-988224	A1	19971210
US 1998-185373	A2	19981103
US 1999-246178	A2	19990204
US 1999-214645	A2	19990927
US 1999-444112	A2	19991122
US 2000-495052	A2	20000131
US 2000-498557	A2	20000204
WO 2000-US3086	A2	20000204
US 2000-522289	A2	20000309
WO 2000-US6497	W	20000309
US 2000-535754	A2	20000327
WO 2000-US8245	A2	20000327
US 2000-594459	A2	20000614
WO 2000-US16838	A2	20000614
US 2000-636778	A2	20000811
US 2000-685432	A2	20001010
US 2000-687219	A3	20001012
WO 2000-US32208	A2	20001122
US 2000-738871	A2	20001215
US 2001-756459	A2	20010108
US 2001-761559	A2	20010116
US 2001-790321	A2	20010221
US 2001-848185	A2	20010503

AB This invention provides methods of obtaining novel polynucleotides and encoded polypeptides by the use of non-stochastic methods of directed evolution (DirectEvolution®). A particular advantage of end-selection-based methods is the ability to recover full-length **polynucleotides** from a **library** of progeny mols. generated by mutagenesis methods. These methods include non-stochastic polynucleotide site-saturation mutagenesis (Gene Site Saturation Mutagenesis®) and non-stochastic polynucleotide reassembly (GeneReassembly®). This invention provides methods of obtaining novel enzymes that have optimized phys. and/or biol. properties. Through use of the claimed methods, genetic vaccines, enzymes, small mols., and other desirable mols. can be evolved towards desirable properties. For example, vaccine vectors can be obtained that exhibit increased efficacy for use as genetic vaccines. Vectors obtained by using the methods can have, for example, enhanced antigen expression, increased uptake into a cell, increased stability in a cell, ability to tailor an immune response, and the like. Furthermore, this invention provides methods of obtaining a variety of novel biol. active mols., in the fields of antibiotics, pharmacotherapeutics, and

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, US, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

AU 9725426	A1	19971017	AU 1997-25426	19970320	
EP 906418	A1	19990407	EP 1997-916943	19970320	

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

JP 2000507444	T2	20000620	JP 1997-534527	19970320	
JP 2001197895	A2	20010724	JP 2000-379523	19970320	
US 6165793	A	20001226	US 1998-75511	19980508	
US 6180406	B1	20010130	US 1998-99015	19980617	
US 6291242	B1	20010918	US 1998-165060	19981002	
US 2002025517	A1	20020228	US 1998-188777	19981109	
US 6391640	B2	20020521			
US 6323030	B1	20011127	US 1999-240310	19990129	
US 6413774	B1	20020702	US 1999-240734	19990129	
US 6573098	B1	20030603	US 1999-240307	19990129	
AU 9923816	A1	19990812	AU 1999-23816	19990416	
AU 747034	B2	20020509			
US 6355484	B1	20020312	US 1999-344002	19990624	
US 6319713	B1	20011120	US 1999-339904	19990625	
US 6309883	B1	20011030	US 2000-490642	20000124	
US 2002051976	A1	20020502	US 2000-559671	20000427	
US 6613514	B2	20030902			
US 6344356	B1	20020205	US 2000-590778	20000608	
US 6372497	B1	20020416	US 2000-590774	20000608	
US 6395547	B1	20020528	US 2000-619550	20000719	
US 6506602	B1	20030114	US 2000-696322	20001025	
US 6518065	B1	20030211	US 2000-696313	20001025	
US 6506603	B1	20030114	US 2000-717391	20001118	
US 6406855	B1	20020618	US 2000-717419	20001122	
US 2003027156	A1	20030206	US 2001-954692	20010912	
US 2003082611	A1	20030501	US 2002-244956	20020917	
US 2003186356	A1	20031002	US 2002-246229	20020917	

PRIORITY APPLN. INFO.:

US 1995-564955	A2	19951130
US 1999-239395	A	19990128
US 1994-198431	A2	19940217
AU 1995-29714	A3	19950217
WO 1995-US2126	A2	19950217
US 1995-425684	A2	19950418
US 1995-537874	A2	19951130
US 1996-537874	A2	19960304
US 1996-621430	B2	19960325
US 1996-621859	A	19960325
WO 1996-US5480	A2	19960418
US 1996-650400	A2	19960520
US 1996-675502	A2	19960703
US 1996-721824	A2	19960927
US 1996-722660	B2	19960927
EP 1996-940934	A3	19961202
JP 1997-520744	A3	19961202
WO 1996-US19256	W	19961202
US 1996-769062	A3	19961218
JP 1997-534527	A3	19970320

Search completed by David Schreiber 308-4292

WO 1997-US4715	W	19970320
US 1998-75511	A1	19980508
US 1998-189103	A1	19981109
US 2000-490643	A1	20000124
US 2000-717391	A1	20001118

AB A method for DNA reassembly after **random** fragmentation, and its application to mutagenesis of nucleic acid sequences by in vitro or in vivo recombination is described. In particular, a method for the production of nucleic acid fragments or polynucleotides encoding mutant proteins is described. The present invention also relates to a method of repeated cycles of mutagenesis, shuffling and selection which allow for the directed mol. evolution in vitro or in vivo of proteins. Using these methods Aequoreas victorias green fluorescent protein was mutagenized to a form with a 45-fold improvement in fluorescence signal. The DNA shuffling method, when applied to arsenate detoxification bacteria, improved arsenate resistance 50-100-fold.

REFERENCE COUNT: 201 THERE ARE 201 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 52 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2001-080687 [09] WPIDS
DOC. NO. NON-CPI: N2001-061427
DOC. NO. CPI: C2001-023263
TITLE: Characterization of genes induced in tick salivary glands during slow feeding phase of blood meal by cloning genes by forming **subtractive** library containing selectively induced mRNA during tick feeding phase.
DERWENT CLASS: B04 C06 D16 S03
INVENTOR(S): BOLLEN, A; GODFROID, E; LEBOULLE, G
PATENT ASSIGNEE(S): (HENO-N) HENOGEN SA; (BOLL-I) BOLLEN A; (GODF-I) GODFROID E; (LEBO-I) LEBOULLE G
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000077198	A2	20001221	(200109)*	EN	77
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2000050558	A	20010102	(200121)		
EP 1187916	A2	20020320	(200227)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
US 2002127235	A1	20020912	(200262)		
JP 2003502039	W	20030121	(200308)		85
US 2003086937	A1	20030508	(200337)		

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000077198	A2	WO 2000-BE61	20000606
AU 2000050558	A	AU 2000-50558	20000606
EP 1187916	A2	EP 2000-934824	20000606

Search completed by David Schreiber 308-4292

		WO 2000-BE61	20000606
US 2002127235 A1	CIP of	WO 2000-BE61	20000606
		US 2001-910430	20010719
JP 2003502039 W		WO 2000-BE61	20000606
		JP 2001-503642	20000606
US 2003086937 A1	CIP of	WO 2000-BE61	20000606
	CIP of	US 2001-910430	20010719
		US 2002-165605	20020607

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2000050558	A	Based on	WO 2000077198
EP 1187916	A2	Based on	WO 2000077198
JP 2003502039	W	Based on	WO 2000077198

PRIORITY APPLN. INFO: GB 1999-13425 19990609
AN 2001-080687 [09] WPIDS
AB WO 200077198 A UPAB: 20010213
NOVELTY - Producing (M1) a library of cDNAs which are induced in the salivary gland of a tick during the tick feeding phase involves selectively cloning mRNAs induced during the tick feeding phase to obtain a corresponding cDNA library and cloning full-length cDNAs corresponding to at least one incomplete cDNA sequence identified in the library obtained.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

(1) a cDNA library (I) obtained from fed tick salivary glands by (M1);

(2) a nucleic acid (II) derived or derivable from (I);

(3) a polynucleotide (III) isolated or isolatable from tick salivary glands which encodes a tick salivary gland polypeptide or its fragments, and any closely related or complementary polynucleotide;

(4) an isolated polypeptide (IV) or its fragment encoded by (III);

(5) variants (V) and fragments of (IV);

(6) an immunological composition or vaccine for inducing an immunological response in a mammalian host to a tick salivary gland polypeptide comprising (II), (III), (IV), epitope bearing fragments, analogs, outer membrane vesicles or cells (attenuated or otherwise) of the above mentioned components, and a carrier;

(7) a therapeutic agent (VI) having anticoagulant or immunomodulatory properties comprising a polypeptide encoded by (III);

(8) a polynucleotide which is identical are sufficiently identical to a fully defined sequence of 194 (S1), 607 (S2), 259 (S3), 170 (S4), 168 (S5), 247 (S6), 261 (S7), 292 (S8), 270 (S9), 316 (S10), 241 (S11), 636 (S12), 432 (S13), 466 (S14), 377 (S15), 1670 (S16), 158 (S17), 146 (S18), 140 (S19), 143 (S20), 140 (S21), 144 (S22), 95 (S23), 1414 (S24), 200 (S25), 241 (S26), 313 (S27), 2417 (S28) or 933 (S29) nucleotide as given in the specification, or its complementary sequence or fragment, for use as a hybridization probe for cDNA clones encoding tick, (preferably Ixodes ricinus, as salivary gland polypeptides, or for isolating clones of other genes similar to tick salivary gland cDNAs;

(9) a diagnostic kit for a disease or susceptibility to a disease comprising:

(a) a tick salivary gland polynucleotide, preferably comprising sequences (S1)-(S28) or (S29) or its fragment;

(b) nucleotide sequence complementary to (a);

(c) a tick salivary gland polypeptide encoded by (S1)-(S28) or (S29);

(d) an antibody to tick salivary gland polypeptide encoded by (S1)-(S28) or (S29);

(e) a phage displaying an antibody to a tick salivary gland polypeptide, preferably to the polypeptide encoded by one of the cDNA sequences (S1)-(S28) or (S29), by which (a)-(d) may comprise a substantial component;

(10) an anti-I. ricinus polypeptide antibody directed against a polypeptide encoded by (II) or (III);

(11) an immunizing agent including an I. ricinus polypeptide such as (IV);

(12) a vector including (II) or (III);

(13) cell lines transfected with the vector of (12); and

(14) hybridoma cell lines expressing (10).

ACTIVITY - Antibacterial; antirheumatic; antiviral.

No supporting biological data is given.

MECHANISM OF ACTION - vaccine.

No supporting biological data is given.

USE - (I) is useful for identifying genes induced during feeding. The therapeutic agent is used alone or in combination with an anti-tick vaccine to prevent the transmission of pathogens carried by the ticks.

(IV) encoded by (S7), (S16) or (S24) or its fragments, is useful in the manufacture of a medicinal agent for use in hematology. (IV) encoded by (S11), (S17), (S19), (S28) or (S29) or its fragments is useful in the preparation of a medical agent for use in transplantation. The polypeptide are also used in the manufacture of a medicinal agent for use in rheumatology and for general treatment.

(IV), or its epitope bearing fragments, analogs, outer membrane vesicles or cells (attenuated or otherwise) are useful for inducing an immunological response in a mammal adequate to produce antibody and/or T cell immune response to protect the animal from bacteria and viruses which could be transmitted during the blood meal of I. ricinus and other related species. The vectors comprising (III) are also useful for inducing immunological response in a mammal by expressing (IV) in vivo in order induce an antibody response to protect the animal from diseases such as Lyme disease, tick encephalitis virus disease etc., (claimed). The polynucleotides and polypeptides may be employed as research reagents and materials for discovery of treatments and diagnostics to animal and human disease.

Dwg.0/2

L21 ANSWER 53 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2000-376592 [32] WPIDS
DOC. NO. NON-CPI: N2000-282725
DOC. NO. CPI: C2000-113994
TITLE: A library of primers for use in characterizing a selected target sequence via a polymerase-catalyzed primer extension reaction.
DERWENT CLASS: B04 D16 T01
INVENTOR(S): CHIN, A M
PATENT ASSIGNEE(S): (SEQU-N) SEQUETECH CORP
COUNTRY COUNT: 20
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000028087	A1	20000518	(200032)*	EN	44

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP

Search completed by David Schreiber 308-4292

Wilder 09/869,891

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000028087 A1		WO 1999-US26431	19991109

PRIORITY APPLN. INFO: US 1998-107760P 19981110
AN 2000-376592 [32] WPIDS
AB WO 200028087 A UPAB: 20000706
NOVELTY - A modified **oligonucleotide** primer (I) (and **library** (II)) for use in characterizing a selected target sequence via a polymerase-catalyzed primer extension reaction, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

(1) a modified oligonucleotide primer (I) for use in characterizing a selected target sequence, via a polymerase catalyzed primer-extension reaction, comprising an oligonucleotide composed of 7-11 nucleotides extending from a 3' end to a 5' end, with a sequence of nucleotide bases complementary to that of a target's selected sequence and a Tm (undefined) greater than or equal to 35 deg. C, where:

(A) at least 3 nucleotides closest to the primer's 3' end are natural nucleotides linked by natural phosphodiester linkages;

(B) among the remaining primer nucleotides, 2 or more adjoining nucleotides are base analogs of natural nucleotide bases and enhance base stacking in a duplex primer-target structure relative to that observed with natural nucleotides; and/or

(C) an intercalating agent is attached to the 5' end of the primer through a linker to allow intercalation of the agent between the 2 adjacent analog bases;

(2) a **library** (II) of modified **oligonucleotide** primers from which can be selected, an oligonucleotide primer (i.e. (I)) for use in characterizing a selected target sequence via a polymerase catalyzed primer-extension reaction;

(3) a method (III) of selecting a modified oligonucleotide primer for use in characterizing a selected target sequence, via a polymerase-catalyzed primer-extension reaction where the target has a known sequence of at least about 100 nucleotides, comprising:

(A) matching a subsequence (or its complement) within the known target sequence with the sequence of a primer (I) in a **library** (II) of **oligonucleotide** primers; and

(B) selecting the matched-sequence primer for use in the primer extension reaction;

(4) a computer-based system (IV) to facilitate selection from a reduced-set **library** (II) of modified **oligonucleotide** primers (I) effective for use in characterizing a selected target sequence, via a polymerase-catalyzed primer-extension reaction where the target has a known sequence of at least about 100 nucleotides, comprising:

(A) a processor; and

(B) a program of instructions for controlling the processor to:

(i) display the reduced-set **library** of **oligonucleotides**;

(ii) enable a user to input a target sequence into the computer system;

(iii) compare the target sequence with primer sequences in the reduced-set **library** (II) of **oligonucleotides** (I) to select at least one primer sequence from the reduced-set library which has a sequence of nucleotide bases complementary to that of a 7-11 nucleotide portion of the target sequence;

Search completed by David Schreiber 308-4292

(iv) enable a user to input a sequence to be **subtracted** into the computer system;

(v) compare the sequence to be **subtracted** with the at least one primer sequence selected in (4Biii) to **subtract** any primer sequences complementary to a selected sequence;

(vi) enable the user to accept or reject the one or more selected and **subtracted** primers; and

(vii) enable the user to provide payment for the one or more selected and **subtracted** primers; and

(5) a computer-readable medium (V) comprising a program for selecting a modified oligonucleotide primer for use in characterizing a selected target sequence, via a polymerase catalyzed primer-extension reaction where the target has a known sequence of at least about 100 nucleotides, said program of instructions comprising instructions for:

(A) displaying the reduced-set **library** of **oligonucleotides**;

(B) enabling a user to input a target sequence into the computer system;

(C) comparing the target sequence with sequences in the reduced-set **library** of **oligonucleotides** to select at least one sequence from the reduced-set library which has a sequence of nucleotide bases complementary to that of a 7-11 nucleotide portion of the target sequence;

(D) enable a user to input a sequence to be **subtracted** into the computer system;

(E) comparing the sequence to be **subtracted** with the at least one primer sequence selected in (5C) to **subtract** any primer sequences complementary to a selected sequence;

(F) enabling the user to accept or reject the one or more selected and **subtracted** primers; and

(G) enabling the user to provide payment the one or more selected and **subtracted** primers.

USE - (I) and (II) may be used for characterizing a selected target sequence via a polymerase-catalyzed primer extension **reaction** (e.g. **polymerase chain reaction** (**PCR**)).

Dwg.0/4

L21 ANSWER 54 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2000-350727 [30] WPIDS
DOC. NO. CPI: C2000-106753
TITLE: Constructing and screening a **library** of **polynucleotide** sequences in filamentous fungal cells by using an episomal replicating AMA1 (autonomous maintenance in Aspergillus)-based plasmid vector.
DERWENT CLASS: B04 D16
INVENTOR(S): VIND, J
PATENT ASSIGNEE(S): (NOVO) NOVO NORDISK AS; (NOVO) NOVOZYMES AS; (NOVO) NOVO-NORDISK AS
COUNTRY COUNT: 90
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000024883	A1	20000504	(200030)*	EN	79

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS

Search completed by David Schreiber 308-4292

LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 9961885 A 20000515 (200039)
EP 1124949 A1 20010822 (200149) EN
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT
RO SE SI
CN 1324402 A 20011128 (200219)
JP 2002528076 W 20020903 (200273) 76

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000024883	A1	WO 1999-DK552	19991013
AU 9961885	A	AU 1999-61885	19991013
EP 1124949	A1	EP 1999-948721	19991013
		WO 1999-DK552	19991013
CN 1324402	A	CN 1999-812660	19991013
JP 2002528076	W	WO 1999-DK552	19991013
		JP 2000-578437	19991013

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9961885	A	Based on	WO 2000024883
EP 1124949	A1	Based on	WO 2000024883
JP 2002528076	W	Based on	WO 2000024883

PRIORITY APPLN. INFO: DK 1999-718 19990525; DK 1998-1375
19981026
AN 2000-350727 [30] WPIDS
AB WO 200024883 A UPAB: 20000624
NOVELTY - A method of constructing and screening a **library** of **polynucleotide** sequences in filamentous fungal cells by using an episomal replicating AMA1 (autonomous maintenance in Aspergillus)-based plasmid vector, is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for the following:

(1) A method (M1) of constructing and selecting or screening a **library** of **polynucleotide** sequences of interest in filamentous fungal cells, comprising:

(a) transforming the fungal cells with a population of DNA vectors, where each vector comprises:

(i) a polynucleotide sequence encoding a fungal selection marker and a fungal replication initiating sequence where the marker and the replication initiating sequence do not vary within the population; and

(ii) a polynucleotide sequence of interest where the population of DNA vectors contains more than one **variant** of the polynucleotide sequence;

(b) cultivating the cells under selection pressure;

(c) selecting or screening for one or more transformants expressing a desired characteristic; and

(d) isolating the transformant(s) of interest;

(2) A method (M2) of constructing and screening or selecting a **library** of **polynucleotide** sequences of interest in a filamentous fungal cell, comprising:

(a) transforming a culture of bacterial or yeast cells with a population of the DNA vectors, where the vector further comprises a

nucleic acid sequence encoding a bacterial or yeast selective marker and a bacterial or yeast replication initiating sequence;

(b) cultivating the bacterial or yeast cells under selection pressure;

(c) isolating the DNA constructs from the transformants of (b);

(d) transforming filamentous fungal cells with the DNA constructs of (c);

(e) cultivating the filamentous fungal cells of (d);

(f) selecting or screening for one or more filamentous fungal transformants expressing a desired characteristic; and

(g) isolating the filamentous fungal transformant(s) of interest; and

(3) A **library** of **polynucleotide** sequences of interest comprising filamentous fungal cells transformed with a population of DNA vectors, where each vector comprising:

(a) a gene encoding a fungal selection marker and a fungal replication initiating sequence where the marker and the replication initiating sequence do not vary within the population; and

(b) a polynucleotide sequence of interest, where the population of DNA vectors contains one or more than one **variant** of the polynucleotide sequence.

USE - The fungal replication initiating sequence is useful in the construction of a **library** of **polynucleotide** sequences of interest (claimed). The methods are useful for constructing and screening a **library** of **polynucleotide** sequences in filamentous fungal cells by using an episomal replicating AMA1-based plasmid vector.

ADVANTAGE - The methods allow a high frequency of transformation which both increases the potential library size and can eliminate the need for library **amplification** in an intermediate host. Also, the properties of the transformants will be uniform.

Dwg.0/4

L21 ANSWER 55 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 2000-350578 [30] WPIDS
CROSS REFERENCE: 2003-511864 [48]
DOC. NO. CPI: C2000-106617
TITLE: Preparing achiral nuclear factor-kappaB specific aptamers for generating high binding, nuclease resistant aptamers that retain their specificity comprises synthesizing amplifying **random** phosphodiester **oligonucleotide** combinatorial **library**.
DERWENT CLASS: B04 D16
INVENTOR(S): ARONSON, J; GORENSTEIN, D G; HERZOG, N; LUXON, B; BRASIER, A R; KING, D J; VENTURA, D A
PATENT ASSIGNEE(S): (TEXA) UNIV TEXAS SYSTEM; (BRAS-I) BRASIER A R; (GORE-I) GORENSTEIN D G; (KING-I) KING D J; (VENT-I) VENTURA D A
COUNTRY COUNT: 86
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000024404	A1	20000504	(200030)*	EN	63
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ TZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZW					
AU 2000013148	A	20000515	(200039)		

obtained.

INDEPENDENT CLAIMS are also included for the following:

(1) an aptamer specific for NF-kB, or a portion, homologous to nine sequences of oligonucleotides, given in the specification, where one or more nucleotides have at least one thiophosphate or dithiophosphate group;

(2) an aptamer specific for NF-kB or constituents comprising a nucleotide sequence homologous to GGGCGTATATG asterisk TGTGGCGGGGG where at least one nucleotide is an achiral thiophosphate or a dithiophosphate;

(3) a method of post-selection aptamer modification comprising:

(a) identifying a first generation target binding aptamer comprising a known sequence of nucleotide bases;

(b) substituting modified achiral nucleotides for one or more selected nucleotides in the sequence, where the substitution results in modified second generation aptamers of the same base sequence as the first generation but with increased nuclease resistance; and

(c) determining the modifications resulting in a relative second generation binding efficiency to the target equal to or greater than the first generation;

(4) an aptamer specific for NF-kB or constituents essentially homologous to the sequences of oligonucleotides consisting of:

(a) single stranded oligonucleotides of 5'-CCAGGAGATTCCAC-3' or 5'-GTGGAATCTCCTGG-3', where between one and six of the nucleotides are diphosphates; and

(b) double stranded oligonucleotides of 5'-CCAGGAGATTCCAC-3' or 5'-GTGGAATCTCCTGG-3', where between one and ten of the nucleotides are diphosphates;

(5) an achiral oligonucleotide that specifically binds a target comprising a sequence of nucleotides, one or more are thiophosphate or dithiophosphate modified;

(6) a process for fractionating oligonucleotides with varying degrees of thiolation comprising:

(a) dissolving a crude thiolated oligonucleotide mixture in a starting solvent;

(b) loading the thiolated oligonucleotide containing solvent onto an anion-exchange column; and

(c) eluting the thiolated oligonucleotide with a buffered solution comprising a salt gradient;

(7) an aptamer prepared by the method above or the method of (3);

(8) a biological chip plate comprising a contiguous substrate to which a selectively partially thiolated aptamer is attached; and

(9) a method of assaying protein:protein or protein:protein:DNA interactions using the biological chip of (8).

USE - The methods are useful for generating high binding, nuclease resistant aptamers that retain their specificity.

Dwg.0/17

L21 ANSWER 56 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2000-206001 [18] WPIDS

CROSS REFERENCE: 2003-093136 [08]; 2003-219980 [21]; 2003-730171 [69]

DOC. NO. CPI: C2000-063714

TITLE: In vitro recombination of polynucleotide fragments to obtain sequences with improved properties involves ligation on an assembly matrix.

DERWENT CLASS: B04 D16

INVENTOR(S): DUPRET, D; LEFEVRE, F; MASSON, J; MASSON, J M

PATENT ASSIGNEE(S): (PROT-N) PROTEUS SA; (DUPR-I) DUPRET D; (LEFE-I) LEFEVRE F; (MASS-I) MASSON J M

COUNTRY COUNT: 87

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000009679	A1	20000224	(200018)*	FR	52
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZA ZW					
FR 2782323	A1	20000218	(200018)		
AU 9951717	A	20000306	(200030)		
EP 1104457	A1	20010606	(200133)	FR	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					
NO 2001005787	A	20011127	(200223)		
JP 2002538763	W	20021119	(200281)		51
US 2003092023	A1	20030515	(200335)		
AU 769516	B	20040129	(200412)		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 2000009679	A1		WO 1999-FR1973	19990811
FR 2782323	A1		FR 1998-10338	19980812
AU 9951717	A		AU 1999-51717	19990811
EP 1104457	A1		EP 1999-936725	19990811
			WO 1999-FR1973	19990811
NO 2001005787	A		WO 1999-FR1973	19990811
			NO 2001-5787	20011127
JP 2002538763	W		WO 1999-FR1973	19990811
			JP 2000-565116	19990811
US 2003092023	A1	CIP of	US 2000-723316	20001128
		Provisional	US 2001-285998P	20010425
		CIP of	US 2001-840861	20010425
			US 2002-153706	20020524
AU 769516	B		AU 1999-51717	19990811

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9951717	A	Based on	WO 2000009679
EP 1104457	A1	Based on	WO 2000009679
JP 2002538763	W	Based on	WO 2000009679
AU 769516	B	Previous Publ.	AU 9951717
		Based on	WO 2000009679

PRIORITY APPLN. INFO: FR 1998-10338 19980812
AN 2000-206001 [18] WPIDS
CR 2003-093136 [08]; 2003-219980 [21]; 2003-730171 [69]
AB WO 200009679 A UPAB: 20040218
NOVELTY - A method (I) for producing recombined **polynucleotide** sequences from a **library** of double-stranded **polynucleotide** sequences is new and comprises fragmenting and denaturing library sequences, hybridizing them with assembly matrices and selecting sequences with requires properties..
DETAILED DESCRIPTION - Method (I) for producing recombined

ZA 2000007261	A	20020731 (200271)	42
AU 761570	B	20030605 (200341)	
NZ 508287	A	20030829 (200365)	

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000000632	A1	WO 1999-US14776	19990629
AU 9948470	A	AU 1999-48470	19990629
NO 2000006675	A	WO 1999-US14776	19990629
		NO 2000-6675	20001228
EP 1092039	A1	EP 1999-932081	19990629
		WO 1999-US14776	19990629
CZ 2000004564	A3	WO 1999-US14776	19990629
		CZ 2000-4564	19990629
CN 1308683	A	CN 1999-807977	19990629
KR 2001071613	A	KR 2000-714838	20001226
JP 2002519038	W	WO 1999-US14776	19990629
		JP 2000-557385	19990629
ZA 2000007261	A	ZA 2000-7261	20001207
AU 761570	B	AU 1999-48470	19990629
NZ 508287	A	NZ 1999-508287	19990629
		WO 1999-US14776	19990629

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9948470	A	Based on	WO 2000000632
EP 1092039	A1	Based on	WO 2000000632
CZ 2000004564	A3	Based on	WO 2000000632
JP 2002519038	W	Based on	WO 2000000632
AU 761570	B	Previous Publ.	AU 9948470
		Based on	WO 2000000632
NZ 508287	A	Based on	WO 2000000632

PRIORITY APPLN. INFO: US 1998-90970P 19980629
AN 2000-137068 [12] WPIDS
AB WO 200000632 A UPAB: 20030919
NOVELTY - A method of generating a nucleic acid library, involving hybridizing single-strand nucleic acid templates to complementary fragments, **amplifying** the fragments to the full length of the templates, and generating an RNA library using RNA polymerase, is new.

DETAILED DESCRIPTION - The method comprises:

(a) providing a population of single-stranded (ss) nucleic acid templates each comprising a coding sequence and an operably linked promoter sequence;

(b) hybridizing to the population of ss nucleic acid templates a mixture of substantially complementary ss nucleic acid fragments shorter in length than the templates;

(c) contacting each of the hybridization products of (b) with both a DNA polymerase which lacks strand displacement activity and a DNA ligase under conditions in which the fragments act as **primers** for the completion of a second nucleic acid strand which is substantially complementary to the nucleic acid template; and

(d) contacting the products of (c) with RNA polymerase to generate an RNA library which is transcribed from the second nucleic acid strand.

INDEPENDENT CLAIMS are also included for the following:

(1) a method for reducing sequence **variation** in a population of nucleic acid molecules, comprising:

(a) providing a first population of ss nucleic acid templates of varying sequence comprising a coding sequence and an operably linked promoter sequence;

(b) hybridizing to the first population a second population of substantially complementary ss nucleic acid fragments shorter in length than the templates, the fragments being of identical sequence;

(c) contacting the hybridization products of (b) with both a DNA polymerase which lacks strand displacement activity and a DNA ligase under conditions in which the fragments act as **primers** for the completion of a second nucleic acid strand which is substantially complementary to the nucleic acid template; and

(d) contacting the products of (c) with RNA polymerase to generate a population of RNA molecule which are transcribed from the second nucleic acid strand and have reduced sequence **variation** relative to the first population of nucleic acid templates.

(2) a method for generating a nucleic acid library, comprising:

(a) providing a population of ss nucleic acid templates each comprising a coding sequence;

(b) providing a population of ss nucleic acid molecules of varying sequence, substantially complementary to the ss nucleic acid templates;

(c) hybridizing the population of (a) and (b) under conditions sufficient to form duplexes; and

(d) contacting the duplexes with one or more excision/repair enzymes under conditions that allow the enzymes to correct mismatched base pairs in the duplexes; and

(3) a method for generating a nucleic acid library, comprising:

(a) providing a population of single-stranded (ss) nucleic acid templates each comprising a coding sequence;

(b) hybridizing to the population of ss nucleic acid templates a mixture of substantially complementary ss nucleic acid fragments shorter in length than the templates;

(c) contacting each of the hybridization products of (b) with both a DNA polymerase which lacks strand displacement activity and a DNA ligase under conditions in which the fragments act as **primers** for the completion of a second nucleic acid strand which is substantially complementary to the nucleic acid template; and

(d) contacting the products of (c) one or more excision/repair enzymes under conditions that allow the enzymes to correct mismatched base pairs in the products.

USE - The methods are used to generate and alter recombinant RNA, DNA and protein libraries. The methods may be used either to introduce mutations into the library, or correct mutation already in the library (claimed). The libraries can be used to facilitate the isolation of useful compounds, including therapeutics, research diagnostics, and agricultural reagents, as well as their coding sequences.

ADVANTAGE - The methods of the invention provide a means for the introduction of mutations into protein libraries in an unbiased fashion, and also provide a technique by which unfavorable mutations may be removed from a library.

Dwg.0/2

L21 ANSWER 58 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2000:308992 BIOSIS
DOCUMENT NUMBER: PREV200000308992
TITLE: Mapping of accessible sites for oligonucleotide hybridization on hepatitis delta virus ribozymes.
AUTHOR(S): Wrzesinski, Jan; Legiewicz, Michal; Ciesiolka, Jerzy

Search completed by David Schreiber 308-4292

[Reprint author]
CORPORATE SOURCE: Institute of Bioorganic Chemistry, Polish Academy of Sciences, Noskowskiego 12/14, 61-704, Poznan, Poland
SOURCE: Nucleic Acids Research, (April 15, 2000) Vol. 28, No. 8, pp. 1785-1793. print.
CODEN: NARHAD. ISSN: 0305-1048.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 19 Jul 2000
Last Updated on STN: 7 Jan 2002

AB Semi-**random** libraries of DNA 6mers and RNase H digestion were applied to search for sites accessible to hybridization on the genomic and antigenomic HDV ribozymes and their 3' truncated derivatives. An approach was proposed to correlate the cleavage sites and most likely sequences of oligomers, members of the **oligonucleotide libraries**, which were engaged in the formation of RNA-DNA hybrids. The predicted positions of oligomers hybridizing to the genomic ribozyme were compared with the fold of polynucleotide chain in the ribozyme crystal structure. The data exemplified the crucial role of target RNA structural features in the binding of antisense oligonucleotides. It turned out that cleavages were induced if the bound oligomer could adapt an ordered helical conformation even when it required partial penetration of an adjacent double-stranded region. The major features of RNA structure disfavoring hybridization and/or RNase H hydrolysis were sharp turns of the polynucleotide chain and breaks in stacking interactions of bases. Based on the predicted positions of oligomers hybridizing to the antigenomic ribozyme we chose and synthesized four antisense DNA 6mers which were shown to direct hydrolysis in the desired, earlier predicted regions of the molecule.

L21 ANSWER 59 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 13
ACCESSION NUMBER: 2000:228171 HCAPLUS
DOCUMENT NUMBER: 133:145742
TITLE: A novel cis-acting element conferring root-preferred gene expression in maize
AUTHOR(S): Lu, Guihua; Bruce, Wesley B.
CORPORATE SOURCE: Pioneer Hi-Bred International, Inc., Johnston, IA, 50131, USA
SOURCE: Journal of Plant Physiology (2000), 156(2), 277-283
CODEN: JPPHEY; ISSN: 0176-1617
PUBLISHER: Urban & Fischer Verlag
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Screening a **random oligonucleotide library** using a modified differential Southwestern method, we generated a root-enriched library of candidate promoter cis-elements that interacted with maize root nuclear proteins. Three candidates that were examined formed root-specific DNA-protein complexes in electrophoretic mobility shift assays. When fused upstream to a synthetic core (SynCore) promoter driving the GUS reporter gene, only one of the three candidates, designated ROL6, generated significantly higher levels of root-preferred expression in particle bombardment-mediated transient assays compared to the SynCore promoter-driven GUS gene. The other two elements showed little or no effect on promoter activity. The addition of the maize Ubi 1 **flanking** region (-865 to -54bp) upstream of the ROL6-SynCore promoter further enhanced root-preferred expression approx. 2-fold over the high level of expression of the maize Ubi 1 promoter alone. Based on public database searches, the ROL6 sequence shows some embedded MYB-binding motifs yet very little homol. to any known plant cis-acting

elements and may contain one or more novel root-preferred cis-acting elements. Overall these results demonstrate first the effectiveness of using this screening approach to isolate functionally active promoter elements and second that ROL6 functions as a root-preferred activator and can be used to modify the expression pattern of transgenes.

REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 60 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:83020 HCAPLUS
DOCUMENT NUMBER: 132:318404
TITLE: Fully Synthetic Human Combinatorial Antibody Libraries (HuCAL) Based on Modular Consensus Frameworks and CDRs **Randomized** with Trinucleotides
AUTHOR(S): Knappik, Achim; Ge, Liming; Honegger, Annemarie; Pack, Peter; Fischer, Melanie; Wellnhofer, Gunter; Hoess, Adolf; Wolle, Joachim; Pluckthun, Andreas; Virnekas, Bernhard
CORPORATE SOURCE: MorphoSys AG, Martinsried/Munich, 82152, Germany
SOURCE: Journal of Molecular Biology (2000), 296(1), 57-86
CODEN: JMOBAK; ISSN: 0022-2836
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB By analyzing the human antibody repertoire in terms of structure, amino acid sequence diversity and germline usage, we found that seven VH and seven VL (four Vκ and three Vλ) germline families cover more than 95 % of the human antibody diversity used. A consensus sequence was derived for each family and optimized for expression in Escherichia coli. In order to make all six complementarity determining regions (CDRs) accessible for diversification, the synthetic genes were designed to be modular and mutually compatible by introducing unique restriction endonuclease sites **flanking** the CDRs. Mol. modeling verified that all canonical classes were present. We could show that all master genes are expressed as soluble proteins in the periplasm of E. coli. A first set of antibody phage display libraries totalling 2+109 members was created after cloning the genes in all 49 combinations into a phagemid vector, itself devoid of the restriction sites in question. Diversity was created by replacing the VH and VL CDR3 regions of the master genes by CDR3 library cassettes, generated from mixed trinucleotides and biased towards natural human antibody CDR3 sequences. The sequencing of 257 members of the unselected libraries indicated that the frequency of correct and thus potentially functional sequences was 61 %. Selection expts. against many antigens yielded a diverse set of binders with high affinities. Due to the modular design of all master genes, either single binders or even pools of binders can now be rapidly optimized without knowledge of the particular sequence, using pre-built CDR cassette libraries. The small number of 49 master genes will allow future improvements to be incorporated quickly, and the separation of the frameworks may help in analyzing why nature has evolved these distinct subfamilies of antibody germline genes. (c) 2000 Academic Press.

REFERENCE COUNT: 120 THERE ARE 120 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 61 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1999:633269 HCAPLUS
DOCUMENT NUMBER: 131:267933
TITLE: A method for sequencing very long DNAs with a small

set of primers that can be mutated and adapted to novel sequence information

INVENTOR(S): Brenner, Sydney
PATENT ASSIGNEE(S): Lynx Therapeutics, Inc., USA
SOURCE: U.S., 28 pp., Cont.-in-part of U.S. 5,780,231.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5962228	A	19991005	US 1997-916120	19970822
US 5763175	A	19980609	US 1995-560313	19951117
US 5780231	A	19980714	US 1996-611155	19960305
JP 11151092	A2	19990608	JP 1998-237840	19980824

PRIORITY APPLN. INFO.: US 1995-560313 A2 19951117
US 1996-611155 A2 19960305
US 1997-916120 A 19970822

AB A novel "primer walking" method for DNA sequencing is provided that uses repeated cycles of nucleotide identification by selective extension and primer advancement along a template by template mutation. An important feature of the invention is providing a set of primers, referred to herein as "rolling primers" that contain complexity-reducing nucleotides for reducing the number of primers required for annealing to every possible primer binding site on a sequencing template. These **primers** have a **defined** 3'-terminal region containing complexity-reducing nucleotides (i.e. bases showing ambiguous base pairing, such as 2'-deoxyinosine), and a 5'-region containing a unique sequence tag that allows it to be captured by a complementary sequence that is part of an ordered array. Another important feature of the invention is the systematic replacement of at least one of the four nucleotides in the target polynucleotide with its cognate complexity-reducing nucleotide or complement thereof. Sequencing is initiated by annealing rolling primers differing only in their terminal nucleotides to a primer binding site of a sequencing template so that only the rolling primer whose terminal nucleotide forms a perfect complement with the template leads to the formation of an extension product. After amplifying the double stranded extension product to form an amplicon, the terminal nucleotide, and hence its complement in the template, is identified by the identity of the amplicon. The primer binding site of the template of the successfully amplified polynucleotide is then mutated by, for example, oligonucleotide-directed mutagenesis so that a subsequent rolling primer may be selected from the set that forms a perfectly matched duplex with the mutated template at a site which is shifted towards the direction of extension by one nucleotide relative to the binding site of the previous rolling primer. The steps of selective extension, amplification and identification are then repeated. In this manner, the primers "roll" along the polynucleotide during the sequencing process, moving a base at a time along the template with each cycle. The procedure may be readily automated for large-scale sequencing projects. Use of inosine as a base in combination with other bases in the 4 3'-terminal bases allows a set of of six primers to act as the progenitors of 200 or more primers that can be generated by mutagenesis as needed.

REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 62 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

Search completed by David Schreiber 308-4292

AU 9923286	A	Based on	WO 9936516
EP 1045899	A2	Based on	WO 9936516
JP 2002508957	W	Based on	WO 9936516
AU 761367	B	Previous Publ.	AU 9923286
		Based on	WO 9936516
AU 2003220702	A1	Div ex	AU 761367

PRIORITY APPLN. INFO: US 1998-8186 19980116; AU 2003-220702 20030718

AN 1999-458459 [38] WPIDS

CR 2000-475913 [41]; 2001-168550 [17]; 2001-168551 [17]; 2001-168564 [17]; 2001-182793 [18]; 2001-624664 [72]; 2002-033177 [04]; 2002-599799 [64]; 2003-220044 [21]; 2003-606536 [57]; 2003-719986 [68]; 2003-720931 [68]

AB WO 9936516 A UPAB: 20040324

NOVELTY - The function of a nucleic acid sequence and the protein it encodes is determined by transfecting the nucleic acid sequence into a host organism and observing any changes that occur.

DETAILED DESCRIPTION - A method (A) of determining the function of a nucleic acid sequence in an organism comprises:

(a) introducing the nucleic acid sequence into a host organism using a viral nucleic acid capable of expressing the nucleic acid sequence; and

(b) observing changes resulting from the expression of the nucleic acid sequence in the organism;

(c) recovering the expressed product of the nucleic acid sequence.

INDEPENDENT CLAIMS are also included for:

(1) functional RNA, DNA, or amino acid sequence molecule recovered according to the method of (A), (B), (C), (D), (G), (H), (I), or (K).

(2) A method (B) of silencing one or more endogenous genes in an organism, a cell or a tissue, comprising introducing a nucleic acid into the organism by way of a viral nucleic acid suitable to express the nucleic acid wherein said nucleic acid is antisense or positive-sense to said endogenous genes. The nucleic acid is especially operable to silence a gene or a multigene family, and the method may further comprise the step of recovering primary or secondary metabolites whose expression is affected by gene silencing.

(3) A method (C) of determining the function of a nucleic acid sequence in an organism comprising:

(a) cloning one or more expressed sequence tag (EST) cDNAs into a viral nucleic acid suitable to produce expression of one or more EST cDNAs in the organism;

(b) transfecting the organism with these constructs; and

(c) observing changes resulting from the expression of the nucleic acid sequence in the organism. The method may further comprise step

(d) recovering the expressed product of the nucleic acid sequence.

(4) A method (D) of determining the function of a nucleic acid sequence in an organism comprising:

(a) altering the genome of a host organism;

(b) introducing a nucleic acid sequence of interest; and

(c) observing changes resulting from expression of the nucleic acid sequence in the organism. The method may further comprise step

(d) recovering the expressed product of the nucleic acid sequence.

(5) A method (E) for identifying a gene function in a transgenic plant carrying a conditional lethal mutation in a gene, comprising:

(a) growing the plant cells (which are especially replica plated plant cells on plant leaf disks) under first permissive conditions;

(b) exposing the plant to restrictive conditions for at least about one growth cycle;

(c) shifting the plant to second permissive conditions for at least

about one growth cycle; and

(d) selecting a plant having a lethal mutation, thereby identifying a plant carrying a lethal mutation that is sensitive to the restrictive condition and essential for survival of the organism. The method may further comprise step

(e) complementing a transgenic plant carrying a recessive or dominant conditional lethal mutation by transfecting with a viral vector containing a functional copy of the mutated gene. The method may further comprise step

(f) isolating from said viral vector a gene correcting or complementing said mutation. Especially, after isolating the gene, the function of the gene is identified, the product expressed by

(6) A method (F) for identifying a gene product target of an antimicrobial drug, herbicide, pesticide or fungicide compound, comprising:

(a) growing plants under first permissive conditions;

(b) exposing the plants to restrictive conditions for a period of time equivalent to at least one growth cycle;

(c) shifting the plants to second permissive conditions for a period of time equivalent to at least one growth cycle;

(d) selecting a plant having a gene carrying a conditional lethal mutation; and

(e) identifying the gene product corresponding to the conditional lethal mutation, thereby identifying a gene product target of a pesticidal or herbicidal compound

(7) A method (G) for constructing an infectious viral vector, comprising inserting one or more nucleotides (especially 1-3 nucleotides) between the transcription start site of a promoter sequence of a viral nucleic acid and the cDNA start site of the viral nucleic acid.

(8) A method (H) for infecting a plant host, comprising transcribing a viral nucleic acid in the absence or presence of a cap analogue.

(9) A method (I) for inhibiting an endogenous protease of a plant host, comprising treating the plant host with a compound, especially jasmonic acid, which induces the production of an endogenous inhibitor of said protease.

(10) A method (J) for improving the expression of a foreign sequence in a plant host, comprising interspecific hybridization.

(11) A method (K) for optimizing the function of a nucleic acid sequence in a plant host, comprising:

(a) constructing a viral expression vector comprising a library containing variants of the nucleic acid sequence;

(b) introducing the viral nucleic acid library into the plant host by expressing variants of the nucleic acid sequence; and

(c) observing changes resulting from the expression of the variants of the nucleic acid sequence. The method may further comprise step

(d) sequencing one or more variants of the nucleic acid sequence.

(12) A method (L) for increasing the representation of nucleic acid sequences in a viral expression library, comprising propagating the library in the absence of E. coli.

(13) A method (M) for determining the function of a gene wherein one or more reporter genes are fused to one or more constitutive or induced promoters in a viral expression vector.

(14) A method (N) for constructing a novel cDNA library from a plant host, comprising:

(a) constructing a viral expression vector containing a non-native nucleic acid sequence;

(b) infecting the plant host with said viral expression vector;

(c) measuring transcription or processing of one or more RNA molecules in the plant host; and

(d) synthesizing said cDNA library from said one or more RNA molecules.

USE - The methods are used to determine the functions of polynucleotides and their encoded proteins (claimed).

ADVANTAGE - The methods of the invention allow the determination of a function of a nucleic acid sequences which has been heretofore unknown.

Dwg.0/28

L21 ANSWER 63 OF 89 MEDLINE on STN DUPLICATE 14
ACCESSION NUMBER: 2000215681 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10752221
TITLE: Oligobodies: bench made synthetic antibodies.
AUTHOR: Radrizzani M; Broccardo M; Gonzalez Solveyra C; Bianchini M; Reyes G B; Cafferata E G; Santa-Coloma T A
CORPORATE SOURCE: Instituto de Investigaciones Bioquimicas-Fundacion Campomar, Buenos Aires, Argentina.
SOURCE: Medicina, (1999) 59 (6) 753-8.
Journal code: 0204271. ISSN: 0025-7680.
PUB. COUNTRY: Argentina
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200004
ENTRY DATE: Entered STN: 20000427
Last Updated on STN: 20000427
Entered Medline: 20000420

AB Using synthetic peptides and a combinatorial **library** of 56 mer **random oligonucleotides**, we have developed reagents that behave as "synthetic antibodies". The results obtained with the protein phosphatase 2A as a model system are shown here. The specificity of these reagents, named "oligobodies", has been demonstrated by Western blot analysis and immunohistochemistry. The oligobodies have enormous advantages compared to antibodies: their production is independent of the immune system, they can be prepared in a few days and there is no need for a purified target protein. These reagents can be produced even if the corresponding protein was never isolated or purified, since only a partial DNA sequence from a database provides enough information to make them.

L21 ANSWER 64 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1999:194474 BIOSIS
DOCUMENT NUMBER: PREV199900194474
TITLE: Site-directed selection of oligonucleotide antagonists by competitive elution.
AUTHOR(S): Bridonneau, Philippe; Chang, Ying-Fon; Velati-Bellini Buvoli, Ada; O'Connell, Dan; Parma, David [Reprint author]
CORPORATE SOURCE: Nexstar Pharmaceuticals, Inc., 2860 Wilderness Place, Boulder, CO, 80301, USA
SOURCE: Antisense and Nucleic Acid Drug Development, (Feb., 1999) Vol. 9, No. 1, pp. 1-11. print.
ISSN: 1087-2906.
DOCUMENT TYPE: Article
LANGUAGE: English
ENTRY DATE: Entered STN: 25 May 1999
Last Updated on STN: 25 May 1999

AB Oligonucleotide ligands that bind a protein or a small molecule of interest are readily isolated by in vitro selection and amplification of rare sequences from combinatorial **libraries** of sequence-**randomized oligonucleotides** (Gold et al., 1995). Classic systematic evolution of ligands by exponential enrichment (SELEX)

protocols are affinity based (Tuerk and Gold, 1990), but because many problems and applications require antagonists, protocols for selecting inhibitors are both desirable and valuable. A widely applicable approach for isolating inhibitors is competitive elution with a molecule that binds the targeted molecule's active or binding site. We have used this approach to isolate antagonists of wheat germ agglutinin (WGA) from a library of 2'NH2-pyrimidine, 2'OH-purine oligonucleotides by elution with N N' N"-triacetylchitotriose, (GlcNAc)3. The highest affinity aptamers have equilibrium dissociation constants of 1 nM-20 nM for WGA, a 103-104-fold improvement relative to (GlcNAc)3, and unlike the carbohydrate, are highly specific. In addition to competiting for binding with (GlcNAc)3, aptamers inhibit WGA-mediated agglutination of sheep erythrocytes, demonstrating that they are able to compete with natural ligands presented on the surfaces of cells. These results illustrate the feasibility of isolating high-affinity, high-specificity antagonists by competitive elution with low molecular weight, relatively low-affinity, and low-specificity small molecules.

L21 ANSWER 65 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:816043 HCAPLUS
DOCUMENT NUMBER: 130:77053
TITLE: High-affinity oligonucleotide ligands to vascular endothelial growth factor (VEGF)
INVENTOR(S): Janjic, Nebojsa; Gold, Larry
PATENT ASSIGNEE(S): Nexstar Pharmaceuticals, Inc., USA
SOURCE: U.S., 64 pp., Cont.-in-part of U.S. 5,475,096.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 127
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5849479	A	19981215	US 1994-233012	19940425
US 5475096	A	19951212	US 1991-714131	19910610
EP 786469	A2	19970730	EP 1997-200035	19910610
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
IL 112141	A1	19980405	IL 1991-112141	19910611
US 5496938	A	19960305	US 1992-964624	19921021
CA 2169536	AA	19950316	CA 1994-2169536	19940908
WO 9507364	A1	19950316	WO 1994-US10306	19940908
W: AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, UZ, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9476865	A1	19950327	AU 1994-76865	19940908
AU 692469	B2	19980611		
EP 724647	A1	19960807	EP 1994-927409	19940908
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 09502354	T2	19970311	JP 1994-508834	19940908
US 5811533	A	19980922	US 1995-447169	19950519
US 5789163	A	19980804	US 1995-487425	19950607
US 6168778	B1	20010102	US 1997-870930	19970606
US 2003198989	A1	20031023	US 2003-408085	20030403
US 2003176680	A1	20030918	US 2003-409565	20030407

PRIORITY APPLN. INFO.: US 1990-536428 B2 19900611
US 1991-714131 A2 19910610

Search completed by David Schreiber 308-4292

R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
JP 2001508660 W 20010703 (200142) 45
AU 745615 B 20020328 (200235)
US 2003077613 A1 20030424 (200330)
EP 1352959 A1 20031015 (200368) EN
R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
EP 988378 B1 20031126 (200402) EN
R: AT BE CH DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
DE 69820054 E 20040108 (200411)

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9832845	A1		WO 1998-GB219	19980126
AU 9857718	A		AU 1998-57718	19980126
EP 988378	A1		EP 1998-901380	19980126
			WO 1998-GB219	19980126
JP 2001508660	W		JP 1998-531742	19980126
			WO 1998-GB219	19980126
AU 745615	B		AU 1998-57718	19980126
US 2003077613	A1	Cont of	WO 1998-GB219	19980126
		Cont of	US 1999-341711	19990921
			US 2002-118100	20020408
EP 1352959	A1	Div ex	EP 1998-901380	19980126
			EP 2003-76606	19980126
EP 988378	B1		EP 1998-901380	19980126
			WO 1998-GB219	19980126
		Related to	EP 2003-76606	19980126
DE 69820054	E		DE 1998-620054	19980126
			EP 1998-901380	19980126
			WO 1998-GB219	19980126

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 9857718	A	Based on	WO 9832845
EP 988378	A1	Based on	WO 9832845
JP 2001508660	W	Based on	WO 9832845
AU 745615	B	Previous Publ.	AU 9857718
		Based on	WO 9832845
EP 1352959	A1	Div ex	EP 988378
EP 988378	B1	Related to	EP 1352959
		Based on	WO 9832845
DE 69820054	E	Based on	EP 988378
		Based on	WO 9832845

PRIORITY APPLN. INFO: GB 1997-1425 19970124
AN 1998-427941 [36] WPIDS
AB WO 9832845 A UPAB: 19981008
Production of a polynucleotide encoding a protein with desired characteristics by incorporating **variant** peptide regions (**variant** motifs) into defined peptide regions (scaffold sequence) comprises: (a) subjecting parent polynucleotide encoding at least 1 protein motif to mutagenesis to create many differently mutated derivatives, or obtaining parent polynucleotide already encoding at least 1 **variant** protein motifs; (b) using pairs of oligonucleotides which represent locations on parent polynucleotide bounding an intervening

variant protein motif as **amplification primers** to **amplify** intervening motif; (c) obtaining single-stranded nucleotide sequences from **amplified** sequences; (d) assembling polynucleotide encoding protein by incorporating sequences from (c) with nucleotide sequence encoding scaffold sequences. The method optionally further comprises expressing resulting protein and screening for desired properties. Also claimed are: (1) polynucleotide encoding protein (especially antibody/antibody fragment) with desired characteristics produced as above; (2) vectors comprising polynucleotide of (1); (3) host cells transformed with vectors of (2), and (4) protein with desired characteristics produced from polynucleotide.

Oligonucleotides are preferably single-stranded, and one of pair linked to member of a specific binding pair (MSBP; e.g. biotin or streptavidin); method may then further comprise isolating **amplified variant** motif by binding MSPB to its specific binding partner. Parent polynucleotide sequence is preferably mutated using error-prone **PCR** and preferably encodes an antibody/antibody fragment.

USE - The method allows production of proteins with altered (especially improved) characteristics by modifying only specific polynucleotide regions, e.g. sequences encoding a protein's functional regions (e.g. loops) or the CDR regions of an antibody (i.e. the regions involved in antigen binding). Protein characteristics which may be altered may be e.g. the ability of antibodies/fragments to specifically bind to antigens or a protein's tertiary structure, affecting binding or secretion. Polynucleotides can be produced which incorporate **variant** motifs which are mutated forms of the parent polynucleotide (e.g. segments encoding mutated CDR regions) or which are derived from polynucleotides encoding proteins with related sequences, e.g. the CDR regions from one antibody may be replaced with those from another. The polynucleotides can be used to produce a **polynucleotide library** (claimed), by inserting them into suitable vectors (claimed); the library can then be screened for a protein of desired characteristics (claimed).

ADVANTAGE - By targeting defined regions for mutagenesis, screening for desired proteins is reduced compared to existing **random** mutagenesis. DNA regions from different clones may also be shuffled, whilst known DNA shuffling technology precludes shuffling of unmutated regions.

Dwg.0/9

L21 ANSWER 67 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1998-480376 [41] WPIDS
CROSS REFERENCE: 1991-325224 [44]; 2003-844460 [78]
DOC. NO. CPI: C1998-145297
TITLE: Mutagenesis of pre-determined gene sequences - useful for systematic changes of pre-determined amino acids to see their effect on protein activity, and to create gene expression libraries.
DERWENT CLASS: B04 D16
INVENTOR(S): CREA, R
PATENT ASSIGNEE(S): (CREA-I) CREA R
COUNTRY COUNT: 1
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
US 5798208	A	19980825	(199841)*		33

Search completed by David Schreiber 308-4292

Wilder 09/869,891

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
US 5798208	A	CIP of	US 1990-505314	19900405
			US 1992-930600	19921102

PRIORITY APPLN. INFO: US 1992-930600 19921102; US 1990-505314 19900405

AN 1998-480376 [41] WPIDS
CR 1991-325224 [44]; 2003-844460 [78]
AB US 5798208 A UPAB: 20031203

Mutagenesis of a gene encoding a protein (I) comprises:

(a) selecting one or more defined region(s) of the amino acid sequence encoded by the gene to be mutagenised;

(b) for each of the region(s), determining one or more amino acid residue(s) to be inserted into positions in the defined region (1);

(c) synthesising without saturation a mixture of oligonucleotides, comprising a nucleotide sequence for each defined region, where each oligonucleotide contains at each sequence position in region (I), either a nucleotide required for synthesis of the protein to be mutagenised, or a nucleotide required for a codon of one of the predetermined amino acid(s), the mixture containing all possible **variant** oligonucleotides according to this criterion; and

(d) generating an expression **library** of cloned genes containing the **oligonucleotides.**

Also claimed are similar methods, but for more than amino acid change.

USE - The methods are used to systematically produce mutations of proteins to provide novel or improved proteins, especially antibodies. Once a domain for mutation has been selected, (degenerate) mutagenesis **primers** (for the domain) are constructed for a specific amino acid. On mutagenesis, e.g. through **polymerase chain reaction** (**PCR**), the degeneracy of the **primers** changes all the amino acids of a particular kind e.g. all prolines, in the domain. By repeating this, the effect of replacing particular kinds of amino acids, especially charged ones most commonly found in catalytic sites, can be seen on the protein when it is expressed. In this way a screening library of cloned mutated genes (claimed) and their proteins can be constructed for optimal/altered activity studies.

ADVANTAGE - Current mutagenesis techniques, to mutate amino acids involved in catalytic activities, rely on prior sequence knowledge, or 'saturation' techniques involving producing large numbers of mutagenesis **primers** to produce a huge, **random** array of mutants. This is expensive and time consuming to produce and screen.

Dwg.0/8

L21 ANSWER 68 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 1998:373387 BIOSIS
DOCUMENT NUMBER: PREV199800373387
TITLE: In vitro selection of functional nucleic acid sequences.
AUTHOR(S): Nieuwlandt, Dan [Reprint author]
CORPORATE SOURCE: NeXstar Pharmaceuticals Inc., Boulder, CO 80301, USA
SOURCE: Horton, R. M. [Editor]; Tait, R. C. [Editor]. (1998) pp. 117-132. Current Innovations in Molecular Biology Series; Genetic engineering with PCR. print.
Publisher: Horizon Press Inc., 156 Fifth Ave., New York, New York 10010, USA. Series: Current Innovations in

Search completed by David Schreiber 308-4292

Molecular Biology Series.
ISBN: 1-898486-05-0 (paper), 1-898486-12-3 (cloth).
DOCUMENT TYPE: Book
Book; (Book Chapter)
LANGUAGE: English
ENTRY DATE: Entered STN: 2 Sep 1998
Last Updated on STN: 2 Sep 1998

L21 ANSWER 69 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:701649 HCAPLUS
DOCUMENT NUMBER: 130:76131
TITLE: Novel Combinatorial Selection of Phosphorothioate Oligonucleotide Aptamers
AUTHOR(S): King, David J.; Ventura, Daniel A.; Brasier, Allan R.; Gorenstein, David G.
CORPORATE SOURCE: Sealy Center for Structural Biology Department of Human Biological Chemistry Genetics and Sealy Center for Molecular Science, University of Texas Medical Branch, Galveston, TX, 77555-1157, USA
SOURCE: Biochemistry (1998), 37(47), 16489-16493
CODEN: BICHAW; ISSN: 0006-2960
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A novel combinatorial approach is described for construction and screening of enhanced nuclease-resistant phosphorothioate DNA "decoys" or "aptamers". Aptamers have been selected that bind tightly to the nuclear factor for human IL6 (NF-IL6), a basic leucine zipper transcription factor involved in the induction of acute-phase responsive and cytokine gene promoters in response to inflammation. Using a **random** combinatorial selection approach and dNTP(αS)'s in the **PCR** amplification, we can select specific thio-substituted agents which have the highest specificity in binding to target NF-IL6. Using a 22-nucleotide-long duplex **random** library, nanomolar binding, specific 22-mer thiophosphate backbone substitution sequences (at dA positions only) were selected. These show a different consensus sequence than normal phosphate backbone CCAAT/enhancer binding protein recognition sites for NF-IL6. Unlike the wild-type 10-mer sequences, which bind 1 protein dimer/duplex, these 22-mer thiophosphate aptamers bind with a stoichiometry of 2 dimers/duplex.
REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 70 OF 89 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 1998:640243 SCISEARCH
THE GENUINE ARTICLE: 111CY
TITLE: Microsatellite markers for typing Aspergillus fumigatus isolates
AUTHOR: BartDelabesse E; Humbert J F; Delabesse E; Bretagne S (Reprint)
CORPORATE SOURCE: HOP HENRI MONDOR, LAB PARASITOL MYCOL, 51 AVE GEN DELATTRE DE TASSIGNY, F-94010 CRETEIL, FRANCE (Reprint); HOP HENRI MONDOR, LAB PARASITOL MYCOL, F-94010 CRETEIL, FRANCE; INRA, STN HYDROBIOL LACUSTRE, THONON LES BAINS, FRANCE; HOP NECKER ENFANTS MALAD, CNRS URA 1461, HEMATOL LAB, PARIS, FRANCE
COUNTRY OF AUTHOR: FRANCE
SOURCE: JOURNAL OF CLINICAL MICROBIOLOGY, (SEP 1998) Vol. 36, No. 9, pp. 2413-2418.

Search completed by David Schreiber 308-4292

Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171.
ISSN: 0095-1137.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 28

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The use of microsatellites as highly polymorphic DMA markers for the typing of isolates of Aspergillus fumigatus was investigated. Four CA repeats were selected by screening an A. fumigatus DNA **library** ,vith a (CA),, **oligonucleotide**. Primers **flanking** these CA repeats were designed to amplify each locus. One primer of each pair was labeled with a fluorophore, and the **PCR** products were analyzed with an automatic sequencer and the GeneScan software. For each primer set and for a given isolate, one band was detected and was assigned to an allele because A. fumigatus is haploid, With 50 clinical isolates, 50 environmental isolates, and 2 reference strains we obtained 12, 11, 10, and 23 different alleles for the four CA microsatellites, respectively (discriminatory power, 0.994), The results were identical by whatever DNA extraction technique was used. Interestingly, no clustering between environmental and clinical isolates was observed, suggesting that every isolate is potentially pathogenic. Microsatellite markers appear suitable for use in large epidemiological studies of invasive aspergillosis.

L21 ANSWER 71 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1998:224840 HCAPLUS
DOCUMENT NUMBER: 128:304488
TITLE: A **definitive** set of oligonucleotide **primers** for amplifying human V regions
AUTHOR(S): Sblattero, Daniele; Bradbury, Andrew
CORPORATE SOURCE: International School for Advanced Studies, Trieste, 34013, Italy
SOURCE: Immunotechnology (1998), 3(4), 271-278
CODEN: IOTEER; ISSN: 1380-2933
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The creation of large diverse phage antibody libraries from natural sources relies on primers which are able to amplify as many V genes as possible. All functional germline V genes have recently been cataloged in a database, V BASE. Previously published primer sets are unable to recognize all these V genes. The design of a human primer set able to recognize all functional human V genes which can be used to create diverse phage antibody libraries. A new set of primers able to recognize all functional V genes were designed using the following criteria: at least 16 bp homol. of the 3' end of the primer to the V gene, no more than 8-fold total degeneracy and min. primer dimer formation. These primers were tested in all possible combinations in PCR using cDNA from human peripheral blood lymphocytes or from human cord blood lymphocytes. By computer anal., all V genes in V BASE could be amplified using this primer set. This theor. result was tested practically by PCR and all primer pairs were shown to be functional, producing PCR products of the expected size. The intensity of the PCR products reflected information available on the expression of the different V gene families recognized and their expression in these two different V gene sources. This new primer set will facilitate the creation of more diverse phage antibody libraries than has been hitherto possible using presently available primer sets.

REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS

AB Methods of identifying exposed sequences in RNAs that can be used as targets for an endogenous RNase H using **libraries** of **oligonucleotides** that are either **random** or exhaustive collections of overlapping sequences derived from the known sequence of the RNA are described. Short oligonucleotides of 7-20 bases are used with a central sequence that will act as part of the substrate with **flanking** oligonucleotides that are modified to protect against nucleases or to increase the stability of the hybrid. A target RNA is incubated with the library and RNase H and any cleavage products arising are amplified and characterized to allow identification of a usable sequence. The method is demonstrated by showing the RNase H cleavage of tumor necrosis factor α mRNA.

L21 ANSWER 74 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1997:467751 HCAPLUS
DOCUMENT NUMBER: 127:76978
TITLE: Methods for generating polynucleotides having desired characteristics by iterative selection and recombination
INVENTOR(S): Stemmer, Willem P. C.; Crameri, Andreas
PATENT ASSIGNEE(S): Affymax Technologies N.V., Neth. Antilles; Stemmer, Willem P. C.; Crameri, Andreas
SOURCE: PCT Int. Appl., 208 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 13
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9720078	A1	19970605	WO 1996-US19256	19961202
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5811238	A	19980922	US 1995-564955	19951130
US 6117679	A	20000912	US 1996-621859	19960325
AU 9710873	A1	19970619	AU 1997-10873	19961202
AU 713952	B2	19991216		
EP 876509	A1	19981111	EP 1996-940934	19961202
EP 876509	B1	20010919		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2000500981	T2	20000202	JP 1997-520744	19961202
AT 205877	E	20011015	AT 1996-940934	19961202
US 6335160	B1	20020101	US 1996-769062	19961218
AU 9923816	A1	19990812	AU 1999-23816	19990416
AU 747034	B2	20020509		

PRIORITY APPLN. INFO.:

US 1995-564955	A	19951130
US 1996-621859	A2	19960325
US 1994-198431	A2	19940217
AU 1995-29714	A3	19950217
WO 1995-US2126	A2	19950217
US 1996-537874	A2	19960304

Search completed by David Schreiber 308-4292

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5407799	A	19950418	US 1993-135317	19931012
CA 2103000	AA	19950513	CA 1993-2103000	19931112
PRIORITY APPLN. INFO.:			US 1989-407238	19890914
			US 1991-779290	19911018

AB **Random** and directed priming methods for determining nucleotide sequences by enzymic sequencing techniques, using libraries of **primers** of lengths 8, 9 or 10 bases, are disclosed. These methods permit direct sequencing of nucleic acids as large as 45,000 base pairs or larger without the necessity for subcloning. Individual **primers** are used repeatedly to prime sequence reactions in many different nucleic acid mols. Libraries containing as few as 10,000 octamers, 14,200 nonamers, or 44,000 decamers would have the capacity to determine the sequence of almost any cosmid DNA. **Random** priming with a **fixed** set of **primers** from a smaller library can also be used to initiate the sequencing of individual nucleic acid mols., with the sequence being completed by directed priming with **primers** from the library. In contrast to **random** cloning techniques, a combined **random** and directed priming strategy is far more efficient.

L21 ANSWER 82 OF 89 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN

ACCESSION NUMBER: 95202590 EMBASE
DOCUMENT NUMBER: 1995202590
TITLE: Identification of novel DNA binding targets and regulatory domains of a murine Tinman homeodomain factor, nkx-2.5.
AUTHOR: Ching Yi Chen; Schwartz R.J.
CORPORATE SOURCE: Dept. of Cell Biology, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, United States
SOURCE: Journal of Biological Chemistry, (1995) 270/26 (15628-15633).
ISSN: 0021-9258 CODEN: JBCHA3
COUNTRY: United States
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 029 Clinical Biochemistry
LANGUAGE: English
SUMMARY LANGUAGE: English

AB A murine cardiac-specific homeodomain gene named csx (Komuro, I., and Izumo. S. (1993) Proc. Natl. Acad. Sci. U. S. A. 90, 8145-8149) and nkx-2.5 (Lints, T. J., Parsons, L. M., Hartley, L., Lyons, I., and Harvey, R. P. (1993) Development 119, 419-431) was identified as a potential vertebrate homologue of Drosophila tinman, a mesoderm determination factor required for insect heart formation (Bodmer, R. (1993) Development 118, 719-729). Bacterial expression of the nkx-2.5 homeodomain allowed us to identify downstream DNA targets from a **library** of **randomly** generated **oligonucleotides**. High affinity nkx-2.5 DNA binding sites, 5'-TNNAGTG-3', represented novel binding sequences, whereas intermediate and weaker affinity sites, 5'-C(A/T)TTAATTN-3', contained the typical 5'-TAAT-3' core required by most homeodomain factors for DNA binding. We also observed that nkx.2.5 served as a modest transcription activator in transfection assays done in 10T1/2 fibroblasts with multimerized binding sites linked to a luciferase reporter gene. Functional dissection of nkx-2.5 revealed a COOH-terminal inhibitory domain composed mainly of clusters of alanines and prolines, which appeared to mask a potent activation domain composed of hydrophobic and highly charged amino acids.

Search completed by David Schreiber 308-4292

[lambda]g11 cDNA inserts into a plasmid vector -- **PCR** cloning using T-vectors -- Thermal cycle dideoxy DNA sequencing -- In vitro mutagenesis -- Ordered deletions using exonuclease III -- Site-directed mutagenesis using a double-stranded DNA template -- Site-directed mutagenesis using a uracil-containing phagemid template -- Construction of linker-scanning mutations by oligonucleotide ligation -- Construction of linker scanning mutations using the **polymerase chain reaction** -- Localized **random polymerase chain reaction** mutagenesis -- Genomic structure -- Simultaneous isolation of RNA and DNA from tissues and cultured cells.
(cont) Physical mapping of the human genome by pulsed field gel electrophoresis -- Field inversion gel electrophoresis -- Enhanced chemiluminescent detection of horseradish peroxidase labeled probes -- Nonradioactive oligonucleotide probe labeling -- Analysis of DNA restriction enzyme digests by two-dimensional electrophoresis in agarose gels -- Inverse **polymerase chain reaction** -- Sequence **variations** -- Use of silver staining to detect nucleic acids -- Nonradioactive method for the detection of single-strand conformational polymorphisms (SSCP) -- Temperature gradient gel electrophoresis (TGGE) for the detection of polymorphic DNA and RNA -- TGGE in quantitative **PCR** of DNA and RNA -- PGK-**PCR** clonality assay (PPCA).
(cont) Direct sequencing of **PCR** products -- Gene expression -- Use of riboprobes for the analysis of gene expression -- Quantification of absolute amounts of cellular messenger RNA by RNA-excess solution hybridization -- Measurements of rate of transcription in isolated nuclei by nuclear run-off assay -- RNA polymerase II in vitro transcription system -- S1 mapping using single-stranded DNA probes -- Single **primer**-mediated **polymerase chain reaction** -- Protein-DNA interactions -- In vivo DNA footprinting by linear **amplification** -- DNA photofootprinting with Rh(phi)2bpy3+ -- Gel retardation assay -- Southwestern assay.
(cont) Cloning DNA binding proteins from cDNA expression **libraries** using **oligonucleotide** binding site probes -- Protein function -- 6xHis-Ni-NTA chromatography as a superior technique in recombinant protein expression/purification -- Production of 35S-labeled proteins in E. coli and their use as molecular probes -- Preparation and ligand screening of a [lambda]g11 lysogen library.

PUB. COUNTRY: New Jersey; United States
DOCUMENT TYPE: Bibliography; (MONOGRAPH)
FILE SEGMENT: U.S. Imprints not USDA, Experiment or Extension
LANGUAGE: English

L21 ANSWER 85 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

Search completed by David Schreiber 308-4292

formula XN, where N is any nucleotide sequence from 5 to 9 nucleotides in length and X is any nucleotide sequence of at least one nucleotide in length that is common to all **oligonucleotide** members in the **library**.
Dwg.0/4

L21 ANSWER 86 OF 89 MEDLINE on STN DUPLICATE 16
ACCESSION NUMBER: 93224151 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8468057
TITLE: A novel zinc finger cDNA with a polymorphic pentanucleotide repeat (ATTTT)n maps on human chromosome 19p.
AUTHOR: Chen H; Kalaitsidaki M; Warren A C; Avramopoulos D; Antonarakis S E
CORPORATE SOURCE: Department of Pediatrics, Johns Hopkins University School of Medicine, Baltimore, Maryland 21287.
CONTRACT NUMBER: HD24605 (NICHD)
HG00373 (NHGRI)
SOURCE: Genomics, (1993 Mar) 15 (3) 621-5.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M99593; GENBANK-U04290; GENBANK-U04291; GENBANK-U04292; GENBANK-U04293; GENBANK-Z22213; GENBANK-Z22214; GENBANK-Z22215; GENBANK-Z22216; GENBANK-Z22217
ENTRY MONTH: 199305
ENTRY DATE: Entered STN: 19930521
Last Updated on STN: 19980206
Entered Medline: 19930511

AB To isolate genes that contain zinc finger motifs, a human brain cDNA **library** was screened with an **oligonucleotide** complementary to the conserved "linker" sequence between adjacent zinc fingers. The insert of one positive clone of 1226 nucleotides contained a novel open reading frame (ZNF121) with 9 zinc finger motifs; in addition, 10 repeats of the pentanucleotide sequence (ATTTT) were found 223 nucleotides after a stop codon and were followed by an Alu repeat. A sequence-tagged site of 172 nucleotides containing this repeat was **defined** by two oligonucleotide **primers**, mapped to chromosome 19 using commercially available mapping panels of hybrid cell lines, and designated D19S204. The pentanucleotide repeat was polymorphic in the members of CEPH families, with 7 alleles ranging in size from 147 to 197 nucleotides. The observed heterozygosity in unrelated CEPH parents was 58% (46 of 79). Genotypes from 34 informative CEPH families were used to perform linkage analyses with other polymorphic markers contained in the CEPH V5 database; strong linkage was found with markers on the short arm of chromosome 19. The zinc finger cDNA described here maps in an area where other zinc finger sequences and multiple cosmid clones containing zinc fingers have been previously localized. The ease of scoring these polymorphic alleles indicates that pentanucleotide repeat polymorphisms may be a particularly useful class of DNA markers for linkage studies.

L21 ANSWER 87 OF 89 MEDLINE on STN DUPLICATE 17
ACCESSION NUMBER: 93147730 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8426111
TITLE: High-frequency representation of a single VH gene in the expressed human B cell repertoire.
COMMENT: Erratum in: J Exp Med. 1993 Apr 1;177(4):1227. PubMed ID:

8459218
AUTHOR: Stewart A K; Huang C; Stollar B D; Schwartz R S
CORPORATE SOURCE: Department of Medicine, New England Medical Center Hospital, Boston, Massachusetts.
CONTRACT NUMBER: AI-26450 (NIAID)
AI-28899 (NIAID)
SOURCE: Journal of experimental medicine, (1993 Feb 1) 177 (2) 409-18.
Journal code: 2985109R. ISSN: 0022-1007.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X67060; GENBANK-X67061; GENBANK-X67062; GENBANK-X67063; GENBANK-X67064; GENBANK-X67065; GENBANK-X67066; GENBANK-X67067; GENBANK-X67068; GENBANK-X67069; GENBANK-X67070; GENBANK-X67071; +
ENTRY MONTH: 199303
ENTRY DATE: Entered STN: 19930312
Last Updated on STN: 19930312
Entered Medline: 19930301

AB Idiotype (Id) 16/6 marks a variable (V) region structure that occurs frequently in the human immunoglobulin repertoire. The basis of the Id has been traced to a germline heavy chain gene segment, VH18/2 (VH26). To pursue the molecular basis for the frequency of Id 16/6, we have analyzed **polymerase chain reaction**-generated C mu, C gamma, and VH3 family V gene libraries derived from the circulating and tonsillar B cells of four normal individuals and from the B cells of two patients with active systemic lupus erythematosus (SLE). The frequency of VH18/2 in these libraries was compared with three control VH genes, VH56P1, VH21/28, and VHA57. Plaque lifts from C mu and C gamma VH cDNA **libraries** were screened with gene-specific **oligonucleotide** probes. The frequency of VH18/2 ranged from 4 to 10% of JH+ plaques (two of five times that of control VH genes). In four VH3 family-specific libraries derived from rearranged DNA, VH18/2 represented 19-33% of VH3+ plaques. Hybridizing VH18/2 plaques were 98-100% homologous to the germline VH gene; mutations when present were often in framework 3. Extensive variation was seen in the complementarity determining region 3 sequences of these rearranged V genes. The high frequency of VH18/2 expression in the B cell repertoire was confirmed by sequencing **randomly** picked JH+ plaques. In two patients with active SLE the frequency of use of VH18/2 was not greater than that observed in normal subjects. These results show that VH18/2 is overrepresented in the B cell repertoire of normal subjects and suggest that the immune repertoire may be dominated by relatively few V genes.

L21 ANSWER 88 OF 89 MEDLINE on STN DUPLICATE 18
ACCESSION NUMBER: 92250034 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1577478
TITLE: Cosmid linking clones localized to the long arm of human chromosome 11.
AUTHOR: Hermanson G G; Lichter P; Selleri L; Ward D C; Evans G A
CORPORATE SOURCE: Molecular Genetics Laboratory, Salk Institute for Biological Studies, La Jolla, California 92037.
SOURCE: Genomics, (1992 May) 13 (1) 134-43.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English

Search completed by David Schreiber 308-4292

FILE SEGMENT: Priority Journals
ENTRY MONTH: 199206
ENTRY DATE: Entered STN: 19920619
Last Updated on STN: 19920619
Entered Medline: 19920605

AB Molecular probes that contain DNA **flanking** CpG-rich restriction sites are extremely valuable in the construction of physical maps of chromosomes and in the identification of genes associated with hypomethylated HTF (HpaII tiny fragment) islands. We describe a new approach to the isolation and characterization of linking clones in arrayed chromosome-specific cosmid libraries through the large-scale semiautomated restriction mapping of cosmid clones. We utilized a cosmid library representing human chromosome 11q12-11qter and carried out automated restriction enzyme analysis, followed by regional localization to chromosome 11q using high-resolution in situ suppression hybridization. Using this approach, 165 cosmid linking clones containing one or more NotI, BssHII, SfiI, or SacII sites were identified among 960 chromosome-specific cosmids. Furthermore, this analysis allowed clones containing a single site to be distinguished from those containing clusters of two or more rare sites. This analysis demonstrated that more than 75% of cosmids containing a rare restriction site also contained a second rare restriction site, suggesting a high degree of CpG-rich restriction site clustering. Thirty chromosome 11q-specific cosmids containing rare CpG-rich restriction sites were regionally localized by high-resolution fluorescence in situ suppression hybridization, demonstrating that all of the CpG-rich sites detected by this method were located in bands 11q13 and 11q23. In addition, the distribution of (CA)n repetitive sequences was determined by hybridization of the arrayed cosmid **library** with **oligonucleotide** probes, confirming a **random** distribution of microsatellites among CpG-rich cosmid clones. This set of reagent cosmid clones will be useful for physical linking of large restriction fragments detected by pulsed-field gel electrophoresis and will provide a new and highly efficient approach to the construction of a physical map of human chromosome 11q.

L21 ANSWER 89 OF 89 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 91:42675 SCISEARCH
THE GENUINE ARTICLE: ER895
TITLE: ISOLATION, CHARACTERIZATION, AND PHYSICAL LOCALIZATION OF 33 HUMAN X-CHROMOSOME RFLP MARKERS
AUTHOR: DIETZBAND J N; TURCO A E; WILLARD H F; VINCENT A; SKOLNICK M H; BARKER D F (Reprint)
CORPORATE SOURCE: UNIV UTAH, DEPT MED INFORMAT, SALT LAKE CITY, UT, 84108; FAC MED STRASBOURG, INST CHIM BIOL, STRASBOURG, FRANCE; STANFORD UNIV, DEPT GENET, STANFORD, CA, 94305
COUNTRY OF AUTHOR: USA; FRANCE
SOURCE: CYTOGENETICS AND CELL GENETICS, (1990) Vol. 54, No. 3-4, pp. 137-141.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 36
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB In a search for highly polymorphic X-specific loci, the X-chromosome DOE Ch35 phage **library** (LAOXNL01) was screened with three **oligonucleotides** representative of minisatellite consensus sequences. A total of 170 clones containing human inserts were isolated by hybridization to the oligonucleotide sequences; each was tested for polymorphism on five **random** female DNAs with six restriction

enzymes. Among the 53 clones demonstrating a polymorphic pattern, 47 were of distinct origin. Twelve of the polymorphisms (23%) were determined to be autosomal. Polymorphisms for the remaining 35 clones were characterized. These polymorphisms represent 33 new X-chromosome RFLP loci, since two pairs of clones detected partially overlapping patterns. A pattern of similar length **variation** with multiple enzymes ("VNTR-type") was demonstrated in 6 (50%) of the 12 non-X-polymorphic clones. However, only 3 (9%) of the 33 X polymorphic loci showed VNTR-like patterns, suggesting a decreased amount of VNTR polymorphism on the X chromosome. The 33 polymorphic X loci were physically localized with a set of rodent x human somatic cell hybrid DNAs representing nine different X-chromosome breakpoints.

Wilder 09/869,891

ACCESSION NUMBER: 1993-336827 [42] WPIDS
CROSS REFERENCE: 1997-118338 [11]; 1999-119881 [10]
DOC. NO. CPI: C1993-149012
TITLE: Oligo nucleotide library - used to produce further oligo nucleotide(s), **primers** etc. of **defined** sequence by simple hybridisation and ligation.
DERWENT CLASS: B04 D16
INVENTOR(S): SHOEMAKER, D; SORGE, J A
PATENT ASSIGNEE(S): (STRA-N) STRATAGENE
COUNTRY COUNT: 19
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9320096	A1	19931014	(199342)*	EN	92
RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
US 5663062	A	19970902	(199741)		17

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9320096	A1		WO 1993-US3230	19930402
US 5663062	A	Cont of	US 1992-863412	19920403
			US 1993-159719	19931130

PRIORITY APPLN. INFO: US 1992-863412 19920403; US 1993-159719 19931130
AN 1993-336827 [42] WPIDS
CR 1997-118338 [11]; 1999-119881 [10]
AB WO 9320096 A UPAB: 19990310
An **oligonucleotide library** (I) is useful for producing an oligonucleotide of preselected sequence. It comprises oligonucleotide members comprising at least 1 species with the formula (X)a(N)b where X is a non-degenerate nucleotide base; N is a degenerate nucleotide base; a is the number of non-degenerate nucleotide positions from 3-8; and b is the number of degenerate positions from 0-4 but not greater than a. Each of the species can form a hybridisation complex with at least one of the other species in the library such that a single ligation event of said complex with another complex results in a ligation reaction prod. of above 12 contiguous nucleotide base pairs.

Also new are (1) a bit for producing an oligonucleotide of preselected sequence comprising, in separate enclosures, one or more of (I) and a suitable ligase or polymerase; and (2) a method for producing an oligonutleotide with a preselected sequence comprising (a) selecting at least 1 oligonucleotide member of (I); (b) hybridising in an aqueous ligation buffer, the member selected in (a); and (c) ligating the resulting ligation reaction substrate from (b) to form a ligation reaction product.

USE/ADVANTAGE - (I) can be used to produce oligonucleotides with a preselected sequence. It uses a non-template dependent method
Dwg.0/7
ABEQ US 5663062 A UPAB: 19971013
A **library** for producing an **oligonucleotide** of preselected nucleotide sequence comprising a number of oligonucleotide members having different nucleotide sequences, each of the oligonucleotide members having the same length and being from 6 to 10 nucleotides in length,the oligonucleotide members all having a sequence according to the

L21 ANSWER 83 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 1994:699102 HCAPLUS
DOCUMENT NUMBER: 121:299102
TITLE: Increasing the diversity of antibody libraries in filamentous phage display libraries using universal or **randomized** immunoglobulin light chains
INVENTOR(S): Barbas, Carlos F.; Burton, Dennis R.; Lerner, Richard A.
PATENT ASSIGNEE(S): Scripps Research Institute, USA
SOURCE: PCT Int. Appl., 121 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 9
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9418219	A1	19940818	WO 1994-US1234	19940202
W: AU, CA, FI, JP, NO				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9461329	A1	19940829	AU 1994-61329	19940202

PRIORITY APPLN. INFO.: US 1993-12566 A 19930202
US 1993-174674 A 19931228
WO 1994-US1234 W 19940202

AB Methods for producing antibody libraries, with increased diversity by mutagenesis within the CDR coding regions of Ig heavy and light chain genes in filamentous phage display libraries is described. **Oligonucleotides** useful for increasing the **library** diversity, and a universal light chain useful in the preparation of the library are described. A mutagenesis method using **PCR** with primers that hybridize to framework coding sequences and contain a **random** sequence of 3-24 triplets is described. A phagemid display vector, pComb3, carrying expression cassettes for heavy and light chain genes leading to surface display of the heavy chain that combined with soluble light chains accumulated in the periplasmic space was constructed using the pelB leader sequence and the cpIII filamentous phage minor coat protein gene. The use of **PCR** with the degenerate primers described above to create antibodies against a number of haptens is demonstrated.

L21 ANSWER 84 OF 89 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2004) on STN
ACCESSION NUMBER: 95:52966 AGRICOLA
DOCUMENT NUMBER: CAT10701058
TITLE: Protocols for gene analysis.
AUTHOR(S): Harwood, Adrian J.
AVAILABILITY: DNAL (QH506.M45 no.31)
LC CONTROL NO.: 94002365
SOURCE: c1994 xiv, 411 p. : ill. ; 23 cm
Publisher: Totowa, N.J. : Humana Press, c1994.
Series: Methods in molecular biology (Clifton, N.J.) ; 31.
ISBN: 0896032582.
NOTE: Includes bibliographical references and index.
Basic recombinant DNA techniques -- Transformation of bacteria by electroporation -- Direct cloning of

RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 72 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
ACCESSION NUMBER: 2003:131965 BIOSIS
DOCUMENT NUMBER: PREV200300131965
TITLE: Identification of differentially regulated sequence-specific DNA-binding activities with a simple oligo selection procedure.
AUTHOR(S): Chen, Zhixiang [Reprint Author]; Wang, Zeping [Reprint Author]; Fan, Baofang [Reprint Author]
CORPORATE SOURCE: Department of Microbiology, Molecular Biology and Biochemistry, University of Idaho, Moscow, ID, USA
SOURCE: Plant Biology (Rockville), (1998) Vol. 1998, pp. 154. print.
Meeting Info.: Annual Meeting of the American Society of Plant Physiologists combined with the 9th International Conference on Arabidopsis Research. Madison, WI, USA. June 27-July 01, 1998. American Society of Plant Physiologists (ASPP).
DOCUMENT TYPE: Conference; (Meeting)
Conference; Abstract; (Meeting Abstract)
LANGUAGE: English
ENTRY DATE: Entered STN: 12 Mar 2003
Last Updated on STN: 12 Mar 2003

L21 ANSWER 73 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 15
ACCESSION NUMBER: 1997:259876 HCAPLUS
DOCUMENT NUMBER: 126:234434
TITLE: Identification of cleavage sites for ribonuclease H on an RNA using **random** or exhaustive **libraries** of **oligonucleotides**
INVENTOR(S): Schmidt, Gunter
PATENT ASSIGNEE(S): Brax Genomics Limited, UK; Schmidt, Gunter
SOURCE: PCT Int. Appl., 45 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT-INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9710332	A2	19970320	WO 1996-GB2275	19960913
WO 9710332	A3	19970515		
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI				
AU 9669394	A1	19970401	AU 1996-69394	19960913
EP 857208	A2	19980812	EP 1996-930282	19960913
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 11514220	T2	19991207	JP 1996-511772	19960913
US 6355418	B1	20020312	US 1998-43149	19980313

PRIORITY APPLN. INFO.: GB 1995-18864 A 19950914
WO 1996-GB2275 W 19960913

Search completed by David Schreiber 308-4292

US 1992-964624	A2	19921021
EP 1991-912753	A3	19910610
IL 1991-98456	A3	19910611
US 1993-117991	A	19930908
US 1993-134028	A	19931007
US 1994-199507	A	19940222
US 1994-205515	B2	19940303
US 1994-233012	A	19940425
US 1994-234997	A	19940428
WO 1994-US10306	W	19940908
US 1995-409442	A1	19950324
US 1995-412110	A1	19950327
US 1995-428964	B1	19950425
US 1995-447169	A2	19950519
US 1995-469609	A1	19950606
US 1998-143190	A1	19980827
US 1998-156824	B1	19980918
US 2000-502344	A1	20000210
US 2001-860474	A1	20010518
US 2001-37986	A1	20011018

AB This invention describes the isolation and characterization of binding properties of a set of high-affinity RNA ligands to vascular endothelial growth factor (VEGF). These ligands were selected from an initial pool of about 1014 RNA mols. **randomized** at thirty contiguous positions. The evolved RNA ligands bind VEGF with affinities in the low nanomolar range. Also described are modified RNA ligands to VEGF. Such modified RNA ligands may be prepared after the identification of 2'-OH RNA ligands or by performing SELEX using a candidate mixture of modified RNAs. For example, 2'-NH2 pyrimidine RNA ligands to VEGF are described. The present invention includes the method of identifying nucleic acid ligands and ligand sequences to VEGF.

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 66 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN
ACCESSION NUMBER: 1998-427941 [36] WPIDS
DOC. NO. CPI: C1998-129126
TITLE: Producing polynucleotide(s) encoding modified proteins - by varying only selected regions of polynucleotide, allows production of proteins with desired characteristics e.g. improved antibodies.
DERWENT CLASS: B04 D16
INVENTOR(S): BORREBAECK, C A K; SOEDERLIND, U H E; SODERLIND, U H E
PATENT ASSIGNEE(S): (BIOI-N) BIOINVENT INT AB; (CRIP-I) CRIPPS J E; (BORR-I) BORREBAECK C A K; (SODE-I) SODERLIND U H E
COUNTRY COUNT: 82
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9832845	A1	19980730	(199836)*	EN	44
RW: AT BE CH DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE GH GM GW HU ID IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW					
AU 9857718	A	19980818	(199851)		
EP 988378	A1	20000329	(200020)	EN	

Search completed by David Schreiber 308-4292

Wilder 09/869,891

ACCESSION NUMBER: 1999-458459 [38] WPIDS
CROSS REFERENCE: 2000-475913 [41]; 2001-168550 [17]; 2001-168551 [17]; 2001-168564 [17]; 2001-182793 [18]; 2001-624664 [72]; 2002-033177 [04]; 2002-599799 [64]; 2003-220044 [21]; 2003-606536 [57]; 2003-719986 [68]; 2003-720931 [68]
DOC. NO. NON-CPI: N1999-342917
DOC. NO. CPI: C1999-134625
TITLE: Determining the function of polynucleotide sequences and their encoded proteins by transfecting them into a host organism.
DERWENT CLASS: B04 C06 D16 P13
INVENTOR(S): DELLA-CIOPPA, G; ERWIN, R L; FITZMAURICE, W P; HANLEY, K M; KUMAGAI, M H; LINDBO, J A; MCGEE, D R; PADGETT, H S; POGUE, G P; DELLA-CIOPPA, G R
PATENT ASSIGNEE(S): (LARG-N) LARGE SCALE BIOLOGY CORP; (BIOS-N) BIOSOURCE TECHNOLOGIES INC; (DELL-I) DELLA-CIOPPA G R; (ERWI-I) ERWIN R L; (KUMA-I) KUMAGAI M H; (MCGE-I) MCGEE D R
COUNTRY COUNT: 85
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9936516	A2	19990722	(199938)*	EN	156
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SZ UG ZW					
W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG US UZ VN YU ZW					
AU 9923286	A	19990802	(199954)		
EP 1045899	A2	20001025	(200055)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
KR 2001040337	A	20010515	(200167)		
JP 2002508957	W	20020326	(200236)		332
AU 761367	B	20030605	(200341)		
US 2003167512	A1	20030904	(200359)		
AU 2003220702	A1	20030814	(200420)#		

APPLICATION DETAILS:

PATENT NO	KIND		APPLICATION	DATE
WO 9936516	A2		WO 1999-US1164	19990115
AU 9923286	A		AU 1999-23286	19990115
EP 1045899	A2		EP 1999-903208	19990115
			WO 1999-US1164	19990115
KR 2001040337	A		KR 2000-707808	20000715
JP 2002508957	W		WO 1999-US1164	19990115
			JP 2000-540219	19990115
AU 761367	B		AU 1999-23286	19990115
US 2003167512	A1	CIP of	US 1998-8186	19980116
		CIP of	US 1999-232170	19990115
		Cont of	US 1999-359305	19990721
			US 2002-236508	20020906
AU 2003220702	A1		AU 2003-220702	20030718

FILING DETAILS:

PATENT NO	KIND	PATENT NO

Search completed by David Schreiber 308-4292

polynucleotide sequences from a **library** of double-stranded **polynucleotide** sequences is new and comprises:

(1) fragmenting the library sequences;

(2) denaturing the fragments, optionally in the presence of one or more assembly matrices;

(3) hybridizing the fragments with one or more assembly matrices, if these were not present in step (b);

(4) ligating the fragments to obtain recombined sequences; and

(5) selecting recombined sequences having advantageous properties compared with one or more reference sequences.

INDEPENDENT CLAIMS are also included for the following:

(1) a recombined polynucleotide sequence obtained and selected by method (I);

(2) a vector containing the sequence of (1);

(3) a host cell transformed with the sequence of (1) or the vector of (2);

(4) a protein encoded by the sequence of (1);

(5) a **library** of **polynucleotide** sequences as in (1), vectors as in (2), cells as in (3) or proteins as in (4).

USE - To optimize the properties of polynucleotide sequences in order to confer an improved phenotype and/or to produce improved proteins.

ADVANTAGE - In contrast to known in-vitro recombination methods, i.e. DNA shuffling (Nature, 370, 141, 1994) and staggered extension process (Nature Biotech., 16, 258, 1998), method (I) does not require a polymerization step to produce recombination, but rather uses ligation on an assembly matrix, which ensures a high degree of fidelity in the course of the recombination events and greatly increases the efficiency with which the fragments are reassembled.

Dwg.0/6

L21 ANSWER 57 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2000-137068 [12] WPIDS

DOC. NO. CPI: C2000-042106

TITLE: Novel methods for generating highly diverse **libraries** used to isolate useful **polynucleotides** and polypeptides.

DERWENT CLASS: B04 C03 D16 J04

INVENTOR(S): KREIDER, B; WAGNER, R; WRIGHT, M C

PATENT ASSIGNEE(S): (PHYL-N) PHYLOS INC

COUNTRY COUNT: 86

PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000000632	A1	20000106	(200012)*	EN	32
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL OA PT SD SE SL SZ UG ZW					
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT UA UG UZ VN YU ZA ZW					
AU 9948470	A	20000117	(200026)		
NO 2000006675	A	20001228	(200115)		
EP 1092039	A1	20010418	(200123)	EN	
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE					
CZ 2000004564	A3	20010613	(200138)		
CN 1308683	A	20010815	(200174)		
KR 2001071613	A	20010728	(200208)		
JP 2002519038	W	20020702	(200246)		26

Search completed by David Schreiber 308-4292

transgenic traits.

L21 ANSWER 51 OF 89 HCAPLUS COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 2000:639148 HCAPLUS
DOCUMENT NUMBER: 133:233552
TITLE: Methods for generating polynucleotides having desired characteristics by iterative selection and recombination
INVENTOR(S): Stemmer, Willem P. C.
PATENT ASSIGNEE(S): Maxygen, Inc., USA
SOURCE: U.S., 106 pp., Cont.-in-part of U.S. 5,811,238.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 13
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6117679	A	20000912	US 1996-621859	19960325
US 5811238	A	19980922	US 1995-564955	19951130
US 5837458	A	19981117	US 1996-650400	19960520
CA 2239099	AA	19970605	CA 1996-2239099	19961202
WO 9720078	A1	19970605	WO 1996-US19256	19961202
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9710873	A1	19970619	AU 1997-10873	19961202
AU 713952	B2	19991216		
EP 876509	A1	19981111	EP 1996-940934	19961202
EP 876509	B1	20010919		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
EP 911396	A2	19990428	EP 1998-122014	19961202
EP 911396	A3	19990506		
EP 911396	B1	20010919		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2000500981	T2	20000202	JP 1997-520744	19961202
JP 2000308490	A2	20001107	JP 1999-267847	19961202
EP 1103606	A2	20010530	EP 2001-103198	19961202
EP 1103606	A3	20010822		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
EP 1138763	A2	20011004	EP 2001-113250	19961202
EP 1138763	A3	20020227		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
AT 205877	E	20011015	AT 1996-940934	19961202
AT 205878	E	20011015	AT 1998-122014	19961202
ES 2164929	T3	20020301	ES 1996-940934	19961202
ES 2165124	T3	20020301	ES 1998-122014	19961202
US 6335160	B1	20020101	US 1996-769062	19961218
WO 9735966	A1	19971002	WO 1997-US4715	19970320

DOC. NO. CPI: C2001-092362
TITLE: Methods for producing functional gene and protein libraries comprises by producing hybrid genes and proteins.
DERWENT CLASS: B04 D16
INVENTOR(S): ARNOLD, F; SIEBER, V; ZHANG, J H
PATENT ASSIGNEE(S): (ARNO-I) ARNOLD F; (CALY) CALIFORNIA INST OF TECHNOLOGY
COUNTRY COUNT: 94
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2001030998	A1	20010503	(200131)*	EN	87
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ NL OA PT SD SE SL SZ TZ UG ZW					
W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CR CU CZ DE DK DM EE ES FI GB GD GE HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW					
AU 2001013508	A	20010508	(200149)		
EP 1228200	A1	20020807	(200259)	EN	
R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT RO SE SI					

APPLICATION-DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2001030998	A1	WO 2000-US29717	20001027
AU 2001013508	A	AU 2001-13508	20001027
EP 1228200	A1	EP 2000-975458	20001027
		WO 2000-US29717	20001027

FILING DETAILS:

PATENT NO	KIND		PATENT NO
AU 2001013508	A	Based on	WO 2001030998
EP 1228200	A1	Based on	WO 2001030998

PRIORITY APPLN. INFO: US 2000-672859 20000928; US 1999-161850P 19991027; US 1999-161852P 19991027; US 2000-672629 20000928

AN 2001-300506 [31] WPIDS

AB WO 200130998 A UPAB: 20011129
NOVELTY - A method (M1) of producing a **polynucleotide library** is new.
DETAILED DESCRIPTION - The method comprises:
(1) preparing a polynucleotide construct comprising at least two parent polynucleotides connected by a linker sequence;
(2) digesting the construct;
(3) selecting fragments of the digested polynucleotide construct which approximate a predetermined size; and
(4) circularizing the selected fragments.
INDEPENDENT CLAIMS are provided for:
(1) producing a protein library (M2) comprising expressing a vector of (M1) in an expression system;
(2) a **polynucleotide library** produced by (M1);
(3) a protein library produced by (M2);

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US 6251604 B1 20010626 US 1999-374274 19990813

EP 1224277 A1 20020724 EP 2000-955470 20000811

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL

PRIORITY APPLN. INFO.: US 1999-374274 A1 19990813

WO 2000-US22078 W 20000811

AB The present invention provides methods of **random** mutagenesis which facilitate **random** insertions and deletions on a target polynucleotide with **random**-sequenced oligonucleotides. The method scan be used to generate **random libraries** of **polynucleotides** (e.g.ribozymes and DNA sequences encoding mutants of genes) and polypeptides (e.g. enzymes and antibodies) and search within the **libraries**, the **polynucleotides** or the polypeptides with desired biol. characteristics under specified environment.

REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L21 ANSWER 37 OF 89 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 2002:71744 BIOSIS

DOCUMENT NUMBER: PREV200200071744

TITLE: **Random** truncation and **amplification** of nucleic acid.

AUTHOR(S): Lietz, Eric [Inventor]

CORPORATE SOURCE: ASSIGNEE: Genopsys, Inc.

PATENT INFORMATION: US 6319694 November 20, 2001

SOURCE: Official Gazette of the United States Patent and Trademark Office Patents, (Nov. 20, 2001) Vol. 1252, No. 3. ftp://ftp.uspto.gov/pub/patdata/. e-file. CODEN: OGUPE7. ISSN: 0098-1133.

DOCUMENT TYPE: Patent

LANGUAGE: English

ENTRY DATE: Entered STN: 16 Jan 2002
Last Updated on STN: 25 Feb 2002

AB A method is provided for producing a **library** of mutagenized **polynucleotides** from a target sequence comprising (a) taking a sample comprising: (i) a target sequence including a section to be mutagenized, (ii) a library of first **primers** where the first **primers** include a first **fixed** sequence and a first unknown sequence 3' to the first **fixed** sequence, the first unknown sequence varying within the library of first **primers**, and (iii) a library of second **primers** where the second **primer** include a second **fixed** sequence that differs from the first **fixed** sequence, and a second unknown sequence 3' to the second **fixed** sequence, the second unknown sequence varying within the library of second **primers**; (b) performing one or more cycles of **primer** extension **amplification** on the sample in the presence of at least one polymerase such that a member of the library of the first **primers** is extended relative to the target sequence; and (c) performing one or more additional cycles of **primer** extension **amplification** on the sample such that a member of the library of the second **primers** is extended relative to the first **primer** that was extended in step (b) to form the **library** of mutagenized **polynucleotides**.

L21 ANSWER 38 OF 89 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

ACCESSION NUMBER: 2002-122019 [16] WPIDS